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Copyright (c) 1993 - 2000
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                                                                                                                           Cholera toxin B/en CTP3 epitope of th Cholera toxin B an Cholera toxin B/en E. coli heat labil
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olera olera olera olera olera li LTB	Escherichia coli v E. coli heat-labil Heat labile toxin E coli verotoxin-1 Sequence of sub-un Synthetic cholera Heat labile entero Cholera toxin B su Amino acid sequenc

ALIGNMENTS

RESULT AAY87461 Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea. 07-SEP-1999; Vibrio cholerae. Escherichia coli. Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:3 03-JUL-2000 (first entry) AAY87461; AAY87461 standard; peptide; 12 Williams NA, Hirst TR; 07-SEP-1998; WO200014114-A1. (UYBR-) UNIV BRISTOL. 16-MAR-2000. Ц 98GB-0019484. 99WO-GB02970. ΑA

EtxB;

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

WPI; 2000-256943/22.

Disclosure; Page 15; 62pp; English.

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RESULT
AAP93498
ID AAPS
В
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Matches 12
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ribosyltransferase activity, while the B subunits (EEXB and CtxB)
facilitate the entry of subunit A into the host cell via the binding and
cross-linking of GM-1 receptors. Although GM-1 binding is responsible
for some of the effects of Etx and Ctx, it has been found that certain
effects of the toxins, such as immunomodulation, are not mediated
through GM-1 binding. The peptides of the invention are fragments of the
beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as
normal EtxB and CtxB subunits, except that they do not bind or cross link
GM-1. They may be used in medicine as an immunomodulator or adjuvant.
Therefore, the peptides may be used in the production of a composition
for treating, preventing and/or modulating a disease associated with an
immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463
                                                                                                                                                                                                                                            05-MAY-1988;
                                                                                                                                                                                                                                                                          05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                                                CTP3 epitope of Cholera toxin B subunit; flagellin fusion protein; vaccine; immunotherapy; ds;
                                                                                                                                                                                                                                                                                                                                                                                                          CTP3 epitope of the Cholera
                                                                                                                     N-PSDB; AAN92414.
                                                                                                                                                                 Marjarian WR,
                                                                                                                                                                                                                                                                                                        16-NOV-1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Btx) and its closely related homologue, cholera toxin (Ctx) from vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit
                                                                         New recombinant flagellin gene including epitope, and expressed fusion proteins, o
                                                                                                                                      WPI; 1989-356496/48
                                                                                                                                                                                                (STRD )
                                                                                                                                                                                                              (PRAX-) PRAXIS BIOLOGICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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12; Conser
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4.6e-05;
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    for heterologous vaccines and for p

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This sequence

corresponds

to the CTP3 epitope of the Cholera

toxin

Q

1 VEVPGSQHIDSQ

Matches

Local Similarity

0;

5.9e-05;

Indels

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Disclosure; fig.4B; 137pp; English.

of antibodies.

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Best Local
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                                                              Sequence
                                                                                               A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica of thyroglobulin) can be used as an orral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                                       Claim 7;
                                                                                                                                                                                                                                          Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conjugate; cholera; B toxin; peptide fragment; microparticulate; inert carrier; modified silica; thyroglobulin; oral vaccine; immunisation; infection; insoluble; digestive tract; antigen; intestines; antibodies; secretory; IgA class.
                                                                                                                                                                                                                                                                                              WPI; 1995-403805/51.
                                                                                                                                                                                                                                                                                                                       Marks
                                                                                                                                                                                                                                                                                                                                               (YEDA ) YEDA RES & DEV CO LTD
                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cholera toxin B antigenic peptide fragment CTP3.
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12; Conserv
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                                                                                                                                                                                                                                  silica
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                                                                                                                                                                                                                                                                                                                       Sela M;
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5.9e-05;
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                       Length 15;
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vevpgsqhidsq

AAY87462 standard; peptide; 21

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AAY87462;

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RESULT AAY87462
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CC for treating, preventing and/or modulating a disease associated with an immunomodulator or adjuvant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 15; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adjuvant; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-JUL-2000
                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                           represent preferred peptides particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulators and for treating diarrhea and which do not bind
                                                                                                                                                                                                                                                                                                                                                                           immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463
represent preferred peptides of the invention, AAY87460 being
      6
                                                             1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2000-256943/22
vevpgsqhidsq 17
                                                                                                                           l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     toxin B/enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                    21
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0019484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder; diarrhoea.
                                                                                                                                                        100.0%;
                                                                                                                              0;
                                                                                                                                                        Score 62;
Pred. No.
                                                                                                                                 Mismatches
                                                                                                                           ; DB 21;
. 8.6e-05;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                         Length 21;
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                                                                                                                           0;
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vevpgsqhidsq

17

6

1 VEVPGSQHIDSQ

Query Match Best Local Matches

l Similarity 12; Conserv

Conservative

0

Mismatches

100.0%;

Score 62; DB 21; Pred. No. 8.6e-05;

Length 21; Indels

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Gaps

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AAY87463
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                                                                                             effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY87463 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                               is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-ribosyltransferase activity, while the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heat labile enterotoxin subunit B; Etabeta-4-alpha-2 loop; GM-1 ganglioside
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli heat labile enterotoxin B-derived peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2000
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                                              particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-256943/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Derivatives of Escherichia coli heat labile enterotoxins useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYBR-) UNIV BRISTOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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   AA;
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Qy
                                                                                                     Matches
                                                               Query Match
                                                                                                                                                                            This sequence is encoded by a fragment of the the plasmid pLPA93 which was used in the production of fimH fusion genes comprising the cholera toxin B subunit inserted into the fimH gene. This insert shows the inclusion of the B subunit into the FimH gene and ifferent position of the hepatitis B virus surface antigen pre-S2 region into a different position of the FimH adhesin of type I fimbriae. Restiction site handles (BgIII-sites) were introduced into the fimH gene, and the foreign epitopes are then inserted in-frame. In the selected positions the insertion of the epitopes did not significantly alter the adhesive function of the FimH protein. The expression of the chameric proteins on the surface of fimbriae on bacterial hosts illustrated the possibility of using bacterial adhesins as general presenters of foreign antigens and epitopes.
                                                                                                                                       epitopes. These chimeric genes may be used in the production of variant FimH adhesins which may be useful for targetting active compounds and microbial cells to locations comprising selected receptors to which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FimH;
FimA;
                                                                                                     Sequence
                                                                                                                              the adhesins bind
                                                                                                                                                                                                                                                                                                                                                                                            Receptor specific bacterial adhesins - use compounds and microbial cells to locations
                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAQ93061.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-275442/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hasty DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric -
Chimeric -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9520657-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues 50-64 of cholera toxin B subunit and FimH 224-226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GXBI-) GX BIOSYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR76748 standard;
                                     Local Similarity hes 12; Conserv
1 VEVPGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             type
FimF;
                                                                                                                                                                                                                                                                                                                                                                   Page 58; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klemm P,
                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 fimbriae; organelle; adhesin; al)
   FimG; receptor binding site; PCR;
                                       Conservative
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                                                                                                      ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94US-0187166
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23
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20..22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor binding site;
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                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molin S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Represents FimH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cholera toxin B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Represents FimH
                                       0;
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                                     Pred. No. 9.0
; Mismatches
                                                               Score 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pallesen
                                     9.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                            useful for targetting ions of receptors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                residue 226"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residue
                                                                DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-D-mannoside residue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sokurenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amplify; ss
                                                              Length
                                     Indels
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                                     Gaps
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DEXXEX

Network polymer which comprises a series of composite E. coli heatlabile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis

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RESULT
AAP50439
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ID AAP3
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                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coll (enterotoxin LT). The medicament may be administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as a vaccine 1-10mg of active cpd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
  01-JAN-1980
                                                                                      AAP50439
                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1983-834645/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Milhaud G, Ra
Guyongruaz A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cholera vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP95426-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence of amino acids 50-75 of the carries an Arg at posns. 67 and 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP30265 standard; Protein; 26 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-NOV-1983
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                                                                                                                                                                                                                                 1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                       vevpgsqhidsq
                                                                                   standard; protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 11; 13pp; French.
                                                                                                                                                                                                                                                                                                                                                                                         26
                                                                                                                                                                                                                                                                             100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Raulais D,
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                         AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Delmas A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82FR-0009167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                therapy; E.coli infection; enterotoxin LT
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                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                             Score 62; DB 4;
Pred. No. 0.00011;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                    Length 26;
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala X39 is Asn or Tyr and X46 is Tyr or Asn. See also AAP504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                Synthetic
                                                                                                                                                                  Heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New synthetic polypeptide(s) for part of E. coli enterotoxin(s useful for vaccination of mammals against the enterotoxin(s)
          WPI; 1985-159230/26
                             Houghten
                                                                   12-DEC-1983;
                                                                                     12-DEC-1984;
                                                                                                                            W08502611-A
                                                                                                                                                                                                                   01-JAN-1980
                                                                                                                                                                                                                                       AAP50436;
                                                                                                                                                                                                                                                         AAP50436 standard;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccination of mammals for protection against the enterotoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houghten RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-DEC-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heat-labile
                                                (SCRI-)
                                                                                                         20-JUN-1985
                                                                                                                                                                                      labile toxin
                                                                                                                                                                                               Network polymer which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCRI-) SCRIPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-DEC-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Page 100; 120pp;
                                                                                                                                                                                                                                                                                                                                               Similarity
12; Conserv
                                                 SCRIPPS
                             RA
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                                                                                                                                                                                    (LT)/heat-stable
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                              Tyr
                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                    83US-0559469
                                                                                     84WO-US02030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83US-0559469
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                                                 CLINIC RES
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                                                                                                                                                                  heat-stable
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                                                                                                                                                                                                                                                                                                                                              Score 62; DE Pred. No. 0.0; Mismatches
                                                                                                                                                                                      toxin
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                                                                                                                                                                  toxin;
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hes 0;
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                                                                                                                                                                                    polypeptide
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                                                                                                                                                                  vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                 is Ala or Glu, AAP50439-57.
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                                                                                                                                                                                    repeating
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                  administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg as
                                                The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be
                                                                                                                                                                Cholera toxin B, sub-unit polypeptide(s) as medicaments - effective against Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                interpolypeptide cystine bonds formed between oxidized Cys residence of the repeating units. This polypeptide may be used in the vaccination of mammals for protection against the enterotoxins composite polypeptide is made by solid phase synthesis or recombinant DNA techniques. X9 is Met or Lys, X12 is Ala or Glu
          a vaccine 1-10mg
                                                                                                                                                                                                                                                        (CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8;
                                                                                                                                 Claim
                                                                                                                                                      cholerae
                                                                                                                                                                                                  WPI; 1983-834645/49.
                                                                                                                                                                                                                       Guyongruaz
                                                                                                                                                                                                                                  Milhaud
                                                                                                                                                                                                                                                                                         26-MAY-1982;
                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                      Cholera vaccine;
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                                                                                                                                                                                                                                                                                                               26-MAY-1983;
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                                                                                                                                8; Page 11; 13pp;
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12; Conserv
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                                                                                                                                                      infections, are
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Arg at
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1, Delmas
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                                                                                                                                                                                                                                                                                                                                                                                                      therapy; E.coli infection;
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          active
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                                                                                                                                                                vaccines and coli and Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                      enterotoxin
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                                                                                                                                                      peptide synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                        B1 subunit which
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                                                                                                                                                                                                                                                                                                        Armstrong
Oomen R,
                                                                                                                                             AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                other molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP-ribosylating toxin; pertussis holotoxin; B-subun active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                 Sequence
                                                                                                                                                                                                                            Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                        New modified forms of pertussis holotoxin - crystalline forms of pertussis holotoxin and
                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                    05-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                            24-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADP-ribosylating toxin (verotoxin-1 B-subunit)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1995
                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD
12
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                                                1 VEVPGSQHIDSQ 12
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12; Conser
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Read
                                                                                                                                      infection.
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                                                                    Conservative
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94US-0251121
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Pred. No.
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                                                                                                                                                                                                                                                                                                                   Klein MH,
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0.00045;
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                                                                                                                                                                                                                                                                                                                   Loosmore
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AAW95226 standard; peptide;

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1 VEVPGSQHIDSQ 12 vevpgsqhidsq

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Mismatches

Indels

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Query Match
Best Local Similarity
"~+~hes 12; Conserv
                                                                                                                             operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties. By analysing the 3-dimensional crystalline structure of the pertussis holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin ansumption peptide used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Read RJ,
Hazes B,
                                                                                       Sequence
                                                                                                                                                                                                                                                                                                     holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox
                                                                                                                                                                                                                                                                                                                                                               A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises:

(1) identification of at least one amino acid (aa) residue of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-579908/49
                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 3; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New method for producing modified pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY41816 standard; peptide; 93
                                                                                                                     invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB (UYAL-) UNIV ALBERTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1995;
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three-dimensional
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Oomen
                                                                                           93
          100.0%; ilarity 100.0%; Conservative 0
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                                                                                           ΑĄ,
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93US-0110947.
94US-0251121.
                                                                                                                                                                                                                                                                                                                                                                                                                                           5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0467974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxin; PT; crystalline pertussis holotoxin; ETA; structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cockle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SA,
                             Score 62; DB 20;
Pred. No. 0.00045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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                                          Length 93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Armstrong
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RESULT 1
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AC AAY6
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AT 17-A
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                                                                                                                                          В
                                                                                                                                                                                                                                                                                            The invention relates to methods of preparing a pertussis holotoxin (PT) CC having a modified biological activity. One method comprises identifying C at least 1 site in a PT that interacts with a molecule that is capable of forming a complex with the holotoxin and which molecule is an effector consicty, cell binding or enzymatic activity of PT. The functional contributes to the contributes to the contributes of crystalline PT, determined by analysing the three dimensional contentified interacting site(s) are identified by analysing the three dimensional contentified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter a biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structure confer have functional and/or structural resemblance to other bacterial confer have functional and/or structural resemblance to other bacterial confer such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the cat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                              Query Match
Best Local :
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites o a molecule with crystalline toxin and modifying the identified site
                17-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong GD, (Oomen RP, Read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural analysis; heat-labile; LT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW95226;
                                          AAY68365;
                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pertussis holotoxin; PT; modified enzyme; ADP-ribosylation; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E. coli heat-labile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAR-1999
                                                                     AAY68365 standard;
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                                                                                                                                                                   1 VEVPGSQHIDSQ 12
                                                                                                                                         vevpgsqhidsq
                                                                                                                                                                                               Similarity
12; Conserv
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                                                                                                                                                                                                  Conservative
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                (first entry)
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40pp; English.
                                                                   Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PT; modified; effector; toxicity; cell binding; tion; toxin; crystalline; X-ray crystallography; interacting site; mitogenicity; adjuvanticity;
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Stein
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PE;
                                                                     93
                                                                                                                                                                                                 0;
                                                                                                                                                                                               Score 62; DE Pred. No. 0.0); Mismatches
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                                                                                                                                                                                              ; DB 20;
. 0.00045;
ches 0;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                             The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAY68385 represent peptides to used in the exemplification of the present invention.
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Best Local S
Matches 12
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24-AUG-1993;
31-MAY-1994;
                                                                                  03-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crystalline form of isolated pertussis holotoxin proteins which have functional resemblance -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Read RJ,
Hazes B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pertussis toxin; heat labile toxin; verotoxin; exotoxin A; holotoxin; diphtheria toxin; ApP-ribosylating toxin; mannose binding protein; infection; crystal structure; X-ray crystallography; detoxification;
                                                                                                           AAB66239;
                                                                                                                                  AAB66239
                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB (UYAL-) UNIV ALBERTA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example
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                                                                                                                                                                                            40 vevpgsqhidsq
                                                                                                                                                                                                                      1 VEVPGSQHIDSQ
                                                                                                                                                                                                                                               12;
                                                        verotoxin-1 B subunit
                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Fig 5; 42pp;
                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stein
Oomen
                                                                                                                                                                                                                                               Conservative
                                                                                 (first entry)
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93US-0110947.
94US-0251121.
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                                                                                                                                                                                               51
                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                  93
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                                                        SEQ
                                                                                                                                                                                                                                            Score 62; DB 21,
Pred. No. 0.00045;
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                                                                                                                                                                                                                                                                     Length 93,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Armstrong
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Pertussis toxin; crystal structure; whooping cough; biological activity; lymphocytosis-promoting factor; histamine-sensitising factor; islet-activating protein.

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Search completed: July 3, 2002, 08:54:57 Job time: 287 sec
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                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative (
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Hazes B,
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24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                             The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promotting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin is the cause of whooping cough following infection by Bordetella pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                       Modifying pertussis holotoxin to produce detoxified PT analogs, comprising analyzing crystalline structure of toxin, to identify sites of toxicity, cell binding or enzyme activity of PT and modifying identified site
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                            Example 3; Fig 5; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-122260/13.
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                                                                    1 VEVPGSQHIDSQ 12
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| 40 vevpgsqhidsq 51
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Stein PE;
                                                                                                                                                                                                      93 AA;
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93US-0110947.
94US-0251121.
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Pred. No. 0.00045;
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                                                                                                                                                         Length 93;
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Result
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Maximum
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Maximum Match 100%
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/B_COMB.pep:*
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US-09-191-0552-21
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Sequence 14, Appl	Sequence 3, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 3, Appli	Sequence 22, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 11, Appl		Sequence 10, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 1, Appli	Patent No. 5194375

ALIGNMENTS

H			US-08 ; Seq; ; Pat
ATTORNEY AGENT INFORMATION: NAME: STEWART, Michael I. REGISTRATION NUMBER: 24,973 REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155 TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 93 amino acids TYPE: amino acid STRANDEDNESS: single	APPLICATION UMBER: US/08/ FILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION UMBER: US 08/ FILING DATE: 24-AUG-1993 PRIOR APPLICATION UNMER: US 08/ APPLICATION NUMBER: US 08/ FILING DATE: 31-MAY-1994	A A A A	Application US/082 156122 156122 READ, Randy J. STEIN, Penelope COCKLE, Stephen OOMEN, Raymond F LOOSMORE, Sheen KLEIN, Michel H ARMSTRONG, Glen HAZES, Bart NVENTION: MODIFIC
73 1038-388	US/08/292,968 US 08/110,947 1993 US 08/251,121 US 08/251,121	University Avenue University Avenue k k Lible SS/MS-DOS SASS #1.0, Version #1.25	192968 E. A. A. D. C. TOXIN

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GENERAL II
Matches .
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Best Local Similarity 100.0%;
Matches 12; Conservative
                                            Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,536
FILING DATE: 06-GUN-1995
APPLICATION NUMBER: US 08/292,968
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NUMBER OF SEQUENCES:
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CITY: Toronto
STATE: Ontario
      y Match 100.0%; Score 62; DB 2; Local Similarity 100.0%; Pred. No. 0.00032; hes 12; Conservative 0; Mismatches 0;
                                                                                                                      TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/467,974 FILING DATE:
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                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 0 FILING DATE: 24-AUG-1993
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                                                                                                          TOPOLOGY:
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Ю. 5965385
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STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
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ARMSTRONG, Glen D.
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                                                                                                          Linear
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Pred. No. 0.00032;
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                                      Length 93;
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RESULT 4
US-08-467-976-26
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                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,973
REPERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (416) 595-1153
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 31-MAX-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
PRIOR APPLICATION NUMBER: US 08/
FILING DATE: 24-AUG-1993
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,536
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CORRESPONDENCE ADDRESS:
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                                                                40 VEVPGSQHIDSQ
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                                                                                 1 VEVPGSQHIDSQ 12
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o. 5977304
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Suite 701, 330 University Avenue
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KLEIN, Michel H.
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Pred. No. 0.00032;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/
FILING DATE: 31 MAY-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:

NAME: STEWART, Michael I.

REGISTRATION NUMBER: 24,97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/467,976
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HAZES, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                         APPLICANT:
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CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                    40 VEVPGSQHIDSQ 51
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STRANDEDNESS: si
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M5G 1R7
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Suite 701, 330 University Avenue
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STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
LOOSMORE, Sheena
READ, Randy J.
STEIN, PeneLope E.
COCKLE, Stephen A.
COMEN, Raymond P.
KLEIN, Michel H.
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24-AUG-1993
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Pred. No.
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; TYPE: PRT; ORGANISM: Vibrio cholerae US-08-952-337-5
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Best Local :
                                                                                                                                                                  SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/952,337 CURRENT FILING DATE: 1998-01-05 EARLIER APPLICATION NUMBER: PCT/SE96/00570 EARLIER FILING DATE: 1996-05-02 EARLIER APPLICATION NUMBER: SE 9501682-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
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                                                                                                                                                                                                            SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                           EARLIER FILING DATE: 1995-05-05
                                                                                                                        LENGTH:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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APPLICATION NUMBER: US 01
FILING DATE: 24-AUG-11994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCE.
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Sim & McBurney
CORRESPONDENCE SIM & McBurney
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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Pred. No. 0.00032;
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APPLICANT: Holmgren, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER APPLICATION NUMBER: SE 9501682-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08472171 Patent No. 5932714
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Best Local Similarity
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Best Local
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                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 102
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCE: 56 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                   APPLICATION NUMBER: US/08/472,171 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
RIOR APPLICATION DATA: APPLICATION NUMBER: (
                                                                                                                                                                                                  COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                 STREET: 330 Un
CITY: Toronto
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                                                                                                                                                                                                                                       STATE:
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5. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                    Ontario
                                                                                                                                                                                                                                                                  E: Sim & McBurney
330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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 US 08/393,334
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US-08-894-526-2
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                                                                                                                                                                        ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
DEFERENCE JOCKET NUMBER: 1038-724 MIS: 1b
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
TYPE: amino acid
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Best Local
                                                                             REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 416-595-1155
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: C. TOYONTO
                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VEVPGSQHIDSQ 12
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50 VEVPGSQHIDSQ 61
                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael REGISTRATION NUMBER: 2
                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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                                             amino acid
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GY: linear
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                                                                103 amino acids
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Klein, Michel H
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                                 linear
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              protein
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100.0%; Pred. No. 0.0
ative 0; Mismatches
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Query Match
Best Local Similarity

100.0%;

Score 62; DB 2; Pred. No. 0.00036;

Length 103;

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US-09-013-047-2
                                                                            RESULT 11
              Sequence 2, Application Patent No. 6140082 GENERAL INFORMATION:
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Best Local 9
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APPLICANT: LOOSMO
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 08/393,334
APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
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 APPLICANT:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                        TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                                                        50 VEVPGSQHIDSQ 61
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                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME:
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12; Conserv
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M5G 1R7
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Klein, Michel H.
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 Loosmore, Sheena M.
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                                                                                                                                                                           100.0%; 50
100.0%; P;
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                                              US/09374597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                              Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.30
                                                                                                                                                                                . 0.00036;
ches 0;
                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                            Length 103;
                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                 0;
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                                                                                                                                                                              Gaps
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Best Local Similarity
Thehes 12; Conserv
                                                                                                                                                                                                                                                       Sequence 21, Application US/09191852
Patent No. 6194560
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
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                                                                     ZIP: 77010
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                          STREET: L..
STREET: L..
CITY: Houston
TMATE: TX
TICA
                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/39.
FILING DATE: FEBRUARY 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                  1 VEVPGSQHIDSQ 12
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50 VEVPGSQHIDSQ 61
                                                                                       COUNTRY: U: 7.1P: 77010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/374,597 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         κι: Canada
M5G 1R7
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GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 amino acids
                                                                                                                                                  1301 McKinney,
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Zealey, Gavin R.
Klein, Michel H.
                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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RY 23, 1995
                                                                                                                                                   Suite 5100
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                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62;
Pred. No.
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APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                     Fulbright & Jaworski L.L.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetically Manipulated Strains Of 56
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Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 0.00036;
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US/09/191,852

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; TOPOLOGY: PCT-US95-13376-21
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PCT-US95-13376-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application PC/TUS9513376 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                           TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: FOX, DAVID L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: PO:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                             NAME: JONES, JOHN W.
REGISTATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 367
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 24-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: FOX, DAVIG L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: ami
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 77027-9095
                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Houston
STATE: TX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Pravel, Hewitt, Kimball & Krieger STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 VEVPGSQHIDSQ 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE:
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                                     amino acid
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                                                                                                             713-850-0165
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                 linear
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Pred. No. 0.00036;
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CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1996-05-02
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
ORGANISM: Vibrio cholerae
US-08-952-337-1
                                                                                                              ; TYPE: PRT
; ORGANISM: Eschcerichia coli
US-08-952-337-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
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                                                                                                                                                                            NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Holmogren, Jan
APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
FILE REFERENCE: 3846/0D758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                             APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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100.0%; Score 62; DB 3; ilarity 100.0%; Pred. No. 0.00044; Conservative 0; Mismatches 0;
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Pred. No. 0.00044;
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Query Match
Best Local Similarity
Matches 12; Conserv

Length 123;

Indels

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Result
No.
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Maximum Match 100%.
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US07_COMB.pep:*
                                                                                                                                                                   Query
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10.532 Million cell updates/sec
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Copyright (c) 1993 - 2000 Comp
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1 US-08-732-371A-1

1 US-08-732-371A-1

1 US-09-786-648-4

1 US-09-786-648-5

US-08-110-947-10

US-08-110-947A-26
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   Sequence
Sequence
                                  Sequence 1, Sequence 1, Sequence 1, Sequence 4, Sequence 5, Sequence 5,
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	44		42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ
39	39	39	39	39	39	40	42	42	42	42	44	56	56	56	56	56	56	56	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62	62
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318	131	115	114	91	7	769	2339	2339	631	101	484	1338	750	461	461	382	382	124	371	371	371	364	351	313	138	138	124	124	124	124	119	116	103	103	103	103	93
	26	19	20	19	21	16	22	21	26	15	16	18	18	18	14	1		21	12	11	ഗ	21	21	21	13	13	18	18	_	Н	22	22	22	12	11	7	σ
PCT-US99-17130-318	-60-171-481-15	-09-595-298A-4	-09-620-394B-4	-09-595-298A-	-09-786-648-2	-09-252-991	-09-816-660-1887	-09-733-089-18	-60-324-109-1996	-09-134-000-37	-09-252-991A-2	US-09-402-100-4	-402-100-	US-09-423-493-2	51-315-	08582-	PCT-US01-08582-3	US-09-760-234-7	8-829-026-	-08-784	08-150-305A-3	-09-756-983-2	-09-756-983-1	-09-756-983	-914-479A-	-08-914-479-2	-09-470-124-5	70-124-5	-US99-30747-5	-US99-30747-5	-09-836-433-	-09-836-433-2	-09-836-433-1	-08-817-906-2	US-08-782-832-15	-08-393-334-	US-08-251-121-26
Sequence 318, App	502,	468,	4327,	470,	æ	e 177		Sequence 18876, A			292	4,	2	2,	e 2,	4,	'n	7,	<u>ა</u>	e 6,	3, A	e 22,	18,	15,	2	e 2, 1	57,	e 55,	57,	55, 1	22,	e 20,	e 14,	e 21,	e 15		Sequence 26, Appl

ALIGNMENTS

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US-09-786-648-3

US-09-786-648-3

US-09-786-648-3

Sequence 3, Application US/09786648

Sequence 3, Application US/09786648

GENERAL INFORMATION:

APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond

TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci

TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci

TITLE OF INVENTION: Adjuvants

FILE REFERENCE: 7438

CURRENT APPLICATION NUMBER: US/09/786,648

CURRENT APPLICATION NUMBER: PCT/GB99/02970

PRIOR APPLICATION NUMBER: PCT/GB99/02970

PRIOR APPLICATION NUMBER: PCT/GB99/02970

PRIOR FILING DATE: 1999-09-07

NUMBER OF SEQ ID NOS: 6

SOFTWARE: MS DOS

SEQ ID NO 3

LENGTH: 12

TYPE: PRT

ORGANISM: E. Coli

FEATURE:

COTHER INFORMATION: human variant E. coli

US-09-786-648-3

Ouery Match

Best Local Similarity 100.0%; Score 62: DB 21; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.00041;
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Matches

12;

Conservative

0,

Mismatches

Indels

0;

Gaps

0

Qy

VEVPGSQHIDSQ 12

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Вb
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                                                                                                                                                                                                                    RESULT
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                                                                                                                                                            Sequence 1, Application US/08732371A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 09-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109519
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REGISTRATION NUMBER: 37,971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                    CORRESPONDENCE ADDRESS:
                                                       TITLE OF INVENTION: VACCINES ITITLE OF INVENTION: INFECTING NUMBER OF SEQUENCES: 6
                                                                                                       APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MARKS, Robert S.

APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST
TITLE OF INVENTION: INFECTING AGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
   STREET:
                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                        1 VEVPGSQHIDSQ 12
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419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                      BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                      VACCINES FOR ORAL IMMUNIZATION AGAINST INFECTING AGENTS
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                                                                                                                                                                                                                                                                                                                                                        Score 62; DB 11;
Pred. No. 0.00053;
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                                                                                                                                                                                                                                                                                                                                                                         Length 15;
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VEVPGSQHIDSQ 17

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; FEATURE:
; LOCATION: 45...65
; OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivabl
; OTHER INFORMATION: human variant E. coli
US-09-786-648-4
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; MOLECULE TYPE:
US-08-732-371A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-786-648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4, Application US/09786648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                             SOFTWARE: MS DOS
SEQ ID NO 4
                                                 Matches
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR ETLING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Williams, Neil Andrew APPLICANT: Hirst, Timothy Raymond TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as TITLE OF INVENTION: Adjuvants FILE REFERENCE: 7438
                                                                                                                                                                                                                              LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 202-737-3528 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                ORGANISM: E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 1
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                               Local Similarity hes 12; Conserv
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nes 12; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
1 VEVPGSQHIDSQ 12
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1 VEVPGSQHIDSQ 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 09-JA
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                                                 Conservative
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                                                                Score 62;
Pred. No.
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Pred. No. 0.00053;
                                                 Mismatches
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                                                                0.00079;
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                                                                              Length 21;
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                                                 Indels
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RESULT 6
US-08-110-947-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Applicat GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/09786648
GENERAL INFORMATION:
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Best Local
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TYPE: PRT
ORGANISM: E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                         APPLICATION NUMBER: US/08
FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                          REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELLEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ID NO 5
TELEFAX: (/--, 89-9456 /
                                                                                                                                                                                                                                                                                                                                                                     STREET:
                     TELEPHONE: (703)
                                                                                          NAME: FALLOW, Charles W
REGISTRATION NUMBER: 28,946
                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 22202-0286
                                                                                                                                                                                                                                                                                                                                    CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity les 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08110947
                                                                                                                                                                                                                                                                                                                                                                     E: Shoemaker and Mattare, Ltd.
Suite 1203 Crystal Plaza I, 2001 Jefferson
Davis Hwy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STEIN, Penelope E
COCKLE, Stephen A
OOMEN, Raymond P
KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                READ, Randy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; ilarity 100.0%; Conservative
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                                                                            1038-303 MIS:jb
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Pred. No.
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...ACTERISTICS:
93 amino acids
...PE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-110-947-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-110-947A-26
; Sequence 26, Application US/08110947A
; GENERAL INFORMATION:
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                          ξQ.
                                                                                                                                  ; STRANDEDNESS: Sit
; TOPOLOGY: linear
US-08-110-947A-26
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                                                                                                                                                                                      TELEFAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 2-
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                           Matches
                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTAL.
ZIP: 22202-0200
ZIP: 22202-0200
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
TWOTTER: TBM PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: OOMEN, I APPLICANT: KLEIN, I TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                          Local Similarity hes 12; Conserv
                                                                                                                                                                                                                                                                                                     NAME: FALLOW, Charles W
REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: Suite 1203 Cr
STREET: Davis Highway
                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/110,947A FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Arlington STATE: Virginia
40 VEVPGSQHIDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 VEVPGSQHIDSQ 51
                                                                                                                                                                                                                                                                       TELEPHONE:
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                            1 VEVPGSQHIDSQ 12
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Y: U.S.A.
                                                                                                                                                                             amino acid
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COCKLE, Stephen A
OOMEN, Raymond P
KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Shoemaker and Mattare, Ltd.
Suite 1203 Crystal Plaza I, 20
                                                     100.0%;
nilarity 100.0%;
Conservative 0
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                                                                                                                                                            single
51
                                                                                                                                                                                                                                                          415-0813
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                                                                                                                                                                                                                            26:
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                                                                      Score 62; DB 5;
Pred. No. 0.0044;
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                                                                                      DB 5; Length 93;
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                                                                                                                                                                                                                                                     Sequence 2, Applicati
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: M5G LK,
ZIP: M5G LK,
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IEM PC CODS/MS-DOS
PC-DOS/MS-DOS
PC-DOS/MS-DOS
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPUTED: COMPUTER: IBM PC COMPUTED: POS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: CURRENT APPLICATION DATA: US/08/251,121
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APPLICANT:
APPLICANT:
APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/251,121
FILING DATE: 31-MAX-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
                                                                           NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 1038-335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                 TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                       APPLICANT: LOOSMORE, Sheena M.
APPLICANT: Yaccob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
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                                                       STREET:
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NTRY: Canada
M5G 1R7
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                                     Toronto
Ontario
7: Canada
                                                       330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: Sim & McBurney
Suite 701, 330 University Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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100.0%; Pr
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Pred. No. 0.0044;
; Mismatches 0;
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Best Local S
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TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimbail & Krieger
STREET: 1477 West Loop South, 10th Floor
                                     REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                            FILING DATE: 24-OCT-1994
ATTORNBY/AGENT INFORMATION:
NAME: Kettelberger Denise M.
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HAG, TATIG A.
TITLE OF INVENTION: PRODUCTION OF AN ORALLY IMMUNOGENIC TITLE OF INVENTION: BACTERIAL PROTEIN IN TRANSGENIC PLAN NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 416-595-1155
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                                                                                                                                                                                                  APPLICATION NUMBER: US/08/782,832 FILING DATE: 13-JAN-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 14.77 V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 77027-9095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Stewart, Michael REGISTRATION NUMBER: 249
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arntzen, Charles J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 62; DB 7; 100.0%; Pred. No. 0.005;
                                                                                                                                                                                                                                                                              Release #1.0, Version #1.25
                                                                                                                                                          US 08/328,716
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SEQUENCE CHARACTERISTICS:

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; TYPE: am1
; TOPOLOGY:
US-08-817-906-21
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                                                                               RESULT
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 12; Conserv
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21, Application US/08817906 GENERAL INFORMATION:
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Best Local Similarity
Matches 12; Conserv
                                              Sequence 14, Application US/09836433
                                                                                                                                                                                                                                                                                                                         TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DALL: 800 CLASSIFICATION: 800 PRIOR APPLICATION DATA: PCT/US95/13376 APPLICATION NUMBER: PCT/US95/13376 APPLICATION NUMBER: 24-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,906
FILING DATE: 08/04/97
                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: FOX, David L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements, APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                            103 amino acids
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Pred. No. 0.005;
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Pred. No.
                                                                                                                                                                                      Mismatches
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US-09-836-433-22
: Sequence 22, Application US/09836433
: GENERAL INFORMATION:
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; ORGANISM: synthetic construct US-09-836-433-22
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                             APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT FILING NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SQC ID NO 22
LENGTH: 119
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMÂTION:
APPLICANT: YUKİ, YOShİKAZU
APPLICANT: YÜKİ, YOShİKAZU
APPLICANT: ÜĞAKA, ShİGEZO
TİTLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
EILE REFERENCE: NOT ASSIGNED
CURRENT APPLICATION UNMER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE FILE REFERENCE: NOT ASSIGNED CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SEQ ID NO 14
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TYPE: PRT
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Pred. No. 0.0057;
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Pred. No.
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Best Local Similarity Matches 12; Conserv

Conservative

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Score 62; DB 22; Pred. No. 0.0059;

Length 119;

Mismatches

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Query Match

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RESULT 15
PCT-US99-30747-55
Sequence 55, Application PC/TUS9930747
Sequence 55, Application PC/TUS9930747
GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/85427
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOMBER: PCT/US99/30747
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia coli
Search completed: July 3, 2002, 09:03:20 Job time: 620 sec
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71 VEVPGSQHIDSQ 82
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Maximum Match 100%
Listing first 45 summaries
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/paa/P

2: /cgn2_6/ptodata/2/paa/U

3: /cgn2_6/ptodata/2/paa/U

4: /cgn2_6/ptodata/2/paa/U

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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
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Sequence 10, Appl
Sequence 13, Appl
Sequence 22, Appl
Sequence 12, Appl
Sequence 17, Appl
Sequence 20, Appl
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ALIGNMENTS

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Sequence 8, Application US/10110364
GENERAL IMPORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Handley, Harold H.
APPLICANT: Haparanta, Tapio
APPLICANT: Haparanta, Tapio
APPLICANT: Haparanta, Tapio
APPLICANT: Haparanta, L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: VARIANT; LOCATION: (1)...(103); LOCATION: (1)...(103); OTHER INFORMATION: CTB variant from NCBI gene bank GI: 998409 US-10-110-364-8
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                    Sequence 10, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBEO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local S
CURRENT APPLICATION NUMBER: US/10/110,364
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                                                                                                                                                                                                                                                                                                                           1 VEVPGSQHIDSQ 12
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50 VEVPGSQHIDSQ 61
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12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 103;
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US-10-110-364-22

Sequence 22, Application US/10110364

GENERAL INFORMATION:
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US-10-110-364-13
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                                                                                                      RESULT
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US-10-110-364-13
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 103
                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/10110364 GENERAL INFORMATION:
APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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PRIOR FILING DATE: 2000-10-05
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PRIOR APPLICATION NUMBER: PCT
PRIOR FILING DATE: 2000-10-05
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                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 103
TYPE: PRT
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                                                                                                                                                                           1 VEVPGSQHIDSQ 12
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                                                                                                                                                          VEVPGSQHIDSQ
                                                                                                                                                                                                                             12;
 Haaparanta, Tapio
Ewalt, Karla L.
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nilarity 100.0%;
Conservative 0
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                                                                                                                                                          61
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3ER: PCT/US00/27607
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Pred. No. 0.
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Pred. No. 0.00021;
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                                                                                                                                                                                                                                                            6; Length 103;
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; NAME/KEY: VARIANT; (105); LCCATION: (1)::(105); COTHER INFORMATION: CTB variant from NCBI gene bank GI: 2781121 (Ogawa; OTHER INFORMATION: 41).
US-10-110-364-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(103)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 494265.
US-10-110-364-22
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Best Local Similarity
Matches 12; Conserv
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PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                        Matches
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
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                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08 NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
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TYPE: PRT
                                                                                                                                                                                                                                                                          LENGTH: 105
TYPE: PRT
ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                             FEATURE:
51
                   1 VEVPGSQHIDSQ 12
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VEVPGSQHIDSQ
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Ewalt, Karla L.
                                                                      100.0%; ilarity 100.0%; Conservative 0;
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62
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                                                                      Score 62; DB 6;
Pred. No. 0.00021;
; Mismatches 0;
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Pred. No. 0.00021;
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                                                                                                         Length 105
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US-10-110-364-17; Sequence 17, Apr

Application US/10110364

RESULT

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GENERAL INFORMATION:

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; NAME/KEY: VARIANT
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 223254.
US-10-110-364-20
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US-10-110-364-20
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Best Local Similarity
Watches 12; Conserv?
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Taplo
APPLICANT: Ewalt, Karla L.
                                                                                                                   Query Match
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                                                                               Matches
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 123
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
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                                                                                 Local Similarity nes 12; Conserva
    70
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                                       1 VEVPGSQHIDSQ 12
VEVPGSQHIDSQ 81
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                                                                                 Conservative
                                                                             100.0%; Score 62; DB 6; 1
100.0%; Pred. No. 0.00025;
htive 0; Mismatches 0;
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Pred. No. 0.00025;
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                                                                                                                     Length 123;
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; TYPE: PRT
; ORGANISM: Vibrio cholera
US-10-110-364-2
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                                                                                                                                                                                    ; NAME/KEY: VARIANT; LOCATION: (1)...(124); COTHER INFORMATION: CTB variant from NCBI gene bank GI: 808900 US-10-110-364-6
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; Sequence 2, Application US/10110364
; GENERAL INFORMATION:
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Best Local S
Matches 12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 124
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
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                                                                            Query Match
Best Local Similarity
Matches · 12; Conserv
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APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/110,364 CURRENT FILING DATE: 2002-04-05 PRIOR APPLICATION NUMBER: PCT/US00/27607 PRIOR FILING DATE: 2000-10-05 PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                         ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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71
                     1 VEVPGSQHIDSQ 12
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VEVPGSQHIDSQ
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12; Conserv
                                                                              Conservative
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82
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                                                                                               100.0%;
                                                                                  0;
                                                                                                    Score 62; DB 6;
Pred. No. 0.00026;
                                                                                  Mismatches
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                                                                                  Indels
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RESULT 10

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                                                                                                                                                                   ; NAME/KEY: VARIANT; LOATION: (1)...(124); LOCATION: (1)...(124); OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1169505 US-10-110-364-16
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Best Local Similarity
Watches 12; Conserva
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NAME/KEY: VARIANT
LOCATION: (1)...(124)
THER INFORMATION: CTB variant from NCBI gene bank GI: 48890 (classic OTHER INFORMATION: 569B).
US-10-110-364-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
US-10-110-364-16
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LENGTH: 124
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
                                                                       Matches
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 124
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/10110364 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Handley, Harold H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                ORGANISM: Escherichia coli
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        1 VEVPGSQHIDSQ 12
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                                                                     Conservative
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                                                                   Score 62; DB 6;
Pred. No. 0.00026;
0; Mismatches 0;
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Pred. No.
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                                                                                                          Length 124;
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; LOCATION: (1)...(124)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 145833.
US-10-110-364-18
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                SEQ ID NO 19
LENGTH: 124
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 124
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Best Local Similarity
                                                                                                                                                       APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karia L.

TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US/07/27607
PRIOR APPLICATION NUMBER: PCT/US/07/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                            PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
                                                                                                                                      PRIOR APPLICATION NUMBER: 60/158,561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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ORGANISM: Escherichia coli
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 VEVPGSQHIDSQ 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/10110364
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Pred. No. 0.00026;
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; FEATURE: ; NAME/KEY: VARIANT ; LOCATION: (1)...(124) ; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1648865 ; OTHER INFORMATION: (LT87). US-10-110-364-19

ORGANISM: Escherichia coli

Query Match Best Local Similarity

100.0%;

Score 62; Pred. No.

DB 6; 0.00026;

Length 124;

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Sequence 21, Application US/10110364

GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2002-10-05
PRIOR FILING DATE: 2000-10-05
LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
FEATURE:
FEATURE:
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 69630.
US-10-110-364-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Escherichia coli;
FEATURE:
NAME/KEY: VARIANT;
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 408996.
US-10-110-364-21
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US-10-110-364-23
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US-10-110-364-21
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                                                                                                                                                                                                                                                                                 Sequence 23, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Happaranta, Tapio
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 21
                                                                                                                                                                                  SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative 0
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PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
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Pred. No. 0.00026;
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Query Match 100.0%; Score 62; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.00026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 VEVPGSQHIDSQ 12
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В

71 VEVPGSQHIDSQ 82

Search completed: July 3, 2002, 09:04:12 Job time: 652 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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and is derived by analysis of
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62
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0.00	XVCDB XVVCB cholera enterotoxin, B chain precursor VC1456 [validated] - N;Alternate names: enterotoxin beta chain C;Species: Vibrio cholerae C;Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_che	5 [validated] - Vibrio cholerae (strain N p-2000 #text_change 02-Feb-2001
Summaries	C;Accession: S14624; S39238; S39241; H82196; JC1078; S; R;Dams, E.; de Wolf, M.; Dierick, W. submitted to the EMBL Data Library, March 1991 A;Description: Correction of the cholera toxin nucleot A;Reference number: S14623 A;Accession: S14624 A;Molecule type: DNA A;Residues: 1-124 CDAM>	nucleotide sequence of the Vibrio chol
results predicted by chance to have a to the score of the result being printed, of the total score distribution.	<pre>A;Cross-references: EMBL:X58786; NID:g48420; PIDN:CAA41593.1; A;Experimental source: strain 2125 R;Lebens, M.; Holmgren, J.</pre>	1593.1; PID:g48422
SUMMARIES	Submitted to the EMBL Data Library, November 1993 A; Description: Structure and arrangement of the Choler. A; Reference number: S39238 A: Accession: S39238	1993 ne Cholera toxin genes in vibrio Cholera
ID Description	A; Molecule type: DNA A: Pasidines: 1-124 / IFBN	
	L:x76390; NID:g433856;	PIDN:CAA53973.1; PID:g433857
C96827 protein F20B17.2 [T14755 hypothetical prote	A;Residues: 1-124 <lew> A;Residues: 1-124 <lew> A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1;</lew></lew>	53976.1; PID:g433861
	R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin,	, R.A.; Gwinn, M.L.; Dodson, R. .; Qin, H.; Dragoi, I.; Sellers
	1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477,483, 2000	
191791 . globerellin 20-0xi S17246 . chorismate synthas F90667 hypothetical prote	A; Tille: DNA sequence of both chromosomes of the chore A; Reference number: A82035; MUID:20406833 A:Accession: H82196	спе спотета расподен утогто спотетае:
hýpothetical zuotin-like r	A;Status: preliminary A;Molecule type: DNA	
	A; Residues: 1-124 <hei> A; Cross-references: GB: AE004224; GB: AE003852; NID: g9655952;</hei>	5952; PIDN:AAF94613.1; GSPDB:GN
	strain N16961; a, Q.J.	
	Chinese Biochem. J. 9, 395-399, 1993 A;Title: Nucleotide sequence analysis of the gene encoding	ding the classical biotype V.ch
S28757 Cytochrome c oxida E84125 hydrolase BH3805 [A; Accession: JC1078 A; Molecule type: DNA	
methylenet catechol :	A; Residues: 1-20, 'Q', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 A; Experimental source: classical biotype strain 569B A; Experimental source: classical biotype strain 569B	57,'T',69-124 <shi></shi>
	Biochim. Biophys. Acta 1090, 139-141, 1991 A;Title: Nucleotide sequence analysis of the CT operon	operon of the Vibrio cholerae classi

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A;Gene: vC1456
A;Map position: 1
C;Complex: the cholera enterotoxin molecule contains thr ciate noncovalently with the subunit B, an aggregate of C;Function:
A;Description: involved in binding of the toxin to cell C;Superfamily: cholera enterotoxin beta chain C;Superfamily: cholera enterotoxin beta chain C;Keywords: enterotoxin; toxin F;1-21/Domain: signal sequence #status predicted <SIG>F;22-124/Product: cholera enterotoxin chain B #status pr F;30-107/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Molecule type: protein
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-8
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-8
R;Takao, T; Watanabe, H; Shimonishi, Y.
Eur. J. Blochem. 146, 503-508, 1985
A;Title: Facile identification of protein sequences by mass sp
A;Reference number: A21910; MUID:85126976
A;Accession: A21910
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124 <TA
A;Experimental source: biotype Inaba 5598
A;Note: Asn-65 was partially deaminated to Asp
C;Comment: The authors translated the codon TCA for residue 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: A05130
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A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Cross-references: GB:X00171; NID:948347; PIDN:CAA24996:1; PIR:COSS, A: Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A; Title: Covalent structure of the beta chain of cholera entered as a chain of cholera entered as a chain of cholera entered as a chain of cholera entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a chain entered as a
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A:Residues: 22-38,'H', 40-42,'N', 44-67,'T', 69,'E',71-90,'N',92-124 <LAI>
A:Residues: 22-38,'H', 40-42,'N', 44-67,'T', 69,'E',71-90,'N',92-124 <LAI>
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A;Molecule type: DNA
A;Residues: 1-38,'H',40-67,'T',69-124 <DA2>
A;Cross-references: EMBL:X58785; NID:g48888;
R;Ma, Q.J.; Liu, C.X.; Xiong, L.S.; Yu, X.Q.
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A; Residues: 22-38, H', 40-41 < MAQ>
R; Mekalanos, J.J.; Swartz, D.J.;
Nature 306, 551-557, 1983
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Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 34, 274-280,
A;Title: B subunit of cholera toxin produced in Escherichia
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A; Accession: PC1010
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A; Residues: I-17, 'C', 19, 'Y', 21-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-122, 'E', 124
A; Cross-references: GB: $60731; NID: 9408994; PIDN: AAC60441.1; PID: 9408996
A; Cross-references: GB: $60731; NID: 9408994; PIDN: AAC60441.1; PID: 9408996
R; Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.
Microb. Pathog. 2, 381-390, 1987
Microb. Pathog. 2, 381-390, 1987
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A;Title: Amino acid sequence of heat-labile enterotoxin from A;Reference number: I53542; MUID:93252225
A;Accession: I67644
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    F; 22-124/Product: F; 30-107/Disulfide
                                                                                                                                                                                        A;Description: the biological activity of the C;Superfamily: cholera enterotoxin beta chain
                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 22-24,'S',26-27,'E',29-63,'K',65-66,'A',68-95,'A',97-122,
A;Experimental source: strain 240-3
C;Complex: the heat-labile enterotoxin molecule contains one A chain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin A;Reference number: A61475; MUID:89180953 A;Accession: A61475
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A; Residues: 1-22 < RE2>
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J. Biol. Chem. 262, 10189-10194, 1987
A;Title: A functional interaction between
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J. Bacteriol. 169, 1352-1357, 1987
A;Title: Evolutionary origin of pathogenic
A;Reference number: A26946; MUID:87137303
A;Accession: B26946
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                                                                                       F;1-21/Domain: signal sequence #status predicted <SIG>
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A;Accession: I41287
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A; Residues: 1-27, 'E'
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heat-labile enterotoxin chain bonds: #status predicted
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wł Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.E.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay, C.A.; Li, J.H.; Li, Y.; Liu, Y.; Liu, S.X.; Liu, Z.A.; Livos, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Reference and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
  hypothetical protein DKFZp564A0122.1 - C;Species: Homo sapiens (man) C;Date: 20-Sep-1999 #sequence_revision
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T14755
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A; Residues: 1-260 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GB: AE005173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein SC2All.21c SC2All.21c - Streptomyces coelicolor
                                                                                                                                                                                                                                                            Query Match
Best Local
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Matches 7; Conserv
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                                                                                                                                                       65 VKVPGKQHVSEK 76
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                                                                                                                                                                                                                                                                                                                                                                        F20B17.2
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70.0%;
                                                                                                                                                                                                                                                            62.9%;
50.0%;
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                                                                                                                                                                                                                                                            Score 39; DB Pred. No. 10;
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                                                                                                                                                                                                                                          Mismatches
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20-Sep-1999 #text_change 20-Sep-1999
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.S.; Maiti, R
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C; Accession: T14755
R; Wambutt, R.; Heubner, D.; Mewes, H.W.; Gass submitted to the Protein Sequence Database, A; Reference number: Z18181
A; Accession: T14755
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A35781
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Best Local Similarity
Grands 6; Conserv
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C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology
F;3-297/Domain: (S)-2-hydroxy-acid oxidase homology <2HY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, I. M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M. Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
C:Accession: H75446
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A; Residues: 1-272 <WAM>
A; Cross-references: EMBL: AL110209
A; Molecule type: mRNA
A; Residues: 1-282 <ERN>
                                               A; Reference number: A35781; A; Accession: A35781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE001954; GB:AE000513; NID:g6458751; PIDN:AAF10604.1; PID:g645A;Experimental source: strain R1
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A; Residues: 1-353 <WHI>
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                                A; Status: preliminary
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Best Local Similarity bo...
""-- hes 6; Conservative
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246 ELPGSEHIE 254
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                                                                                                                                                                                                                                                                                                                                                Conservative
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66.7%;
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75.0%;
                                                                  and neurotrophic; MUID:90319130
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ed. No. 11;
Mismatches
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GB:M34643

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C;Geneti
A;Gene:
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A;Title: The primary structure of the subunits of carbon monoxide dehydrogenase/acetyl-CA;Reference number: A41670; MUID:92084676
A;Accession: A41670
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A;Title: Neurotrophin-3: a neurotrophic factor related to NGF and BDNF.
A;Reference number: A40094; MUID:90208301
A;Status: preliminary
                                                                         A;Cross-references: GB:AE005174; NID:g12513064; PIDN:AAG54606.1; GSPDB:GN00145; UWGP:ZO:
A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-352 <STO>
                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 28-Jul-2000
C;Accession: A41670
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Best Local
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les 6; Conserv
Z0347
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R;Jones, D.G.L.; Reusser, U.; Braus, G.H. Mol. Microbiol. 5, 2143-2152, 1991
A;Title: Molecular cloning, characterizat: A;Reference number: $17246; MUID:92114793
A;Accession: $17246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Tanaka-Ueguchi, M.; Itoh, H.; Oyama, N.; Koshioka, M.; Matsuoka, M. submitted to the EMBL Data Library, July 1998
A;Description: Over-expression of a tobacco homeobox gene, NTH15, decreases A;Reference number: Z14418
A;Accession: T01751
C; Keywords: phosphorus-oxygen lyase; tro
F;347-363/Domain: transmembrane #status
                                                                                                                                                      A;Cross-references: EMBL:Z72670; NID:g1322731; PIDN:CAA96860.1; PID:g1322732; GSPDB:GA;Experimental source: strain S288C
                                          C; Superfamily: chorismate synthase
                                                               A; Map position:
                                                                                                            A; Gene: SGD: ARO2; MIPS: YGL148w
                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-376 < VOL>
                                                                                                                                                                                                                                                  A; Reference number: S64153
A; Accession: S64162
                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X60190; NID:g3386; PIDN:CAA42745.1; R;Volckaert, G.; Voet, M.; Verhasselt, P.; Defoor, E. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-376 < JON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: S17246; S64162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chorismate synthase (EC 4.6.1.4) - yeast (Saccharomyces cerevisiae) N;Alternate names: protein G2501; protein YGL148w
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C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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A; Residues: 1-367 <TAN>
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C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
                                                                                  A;Cross-references: SGD:S0003116; MIPS:YGL148w
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: G96554
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G96554
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Best Local Similarity
"-+-hes 6; Conserv?
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F19C24.16 [imported] - Arabidopsis thaliana c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96554
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A;Residues: 1-378 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB33733.1; PID:g13359767; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-423 <STO>
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                                                                                 Local Similarity hes 6; Conserv
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                                                                                                  DB . 42;
                                                                                                                                                                                                                                             PIDN:AAG29686.1; GSPDB:GN00141
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R.Miller, N.; Beck, C.; Kramer, J.
submitted to the EMEL Data Library, June 1997
A; Description: The sequence of A. thaliana IG002P16
A; Reference number: Z14421
A; Accession: T01770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein A_IG002P16.9 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 22-Oct-1999
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A; Molecule type: DNA
A; Residues: 89-442 <WOO>
A; Cross-references: EMBL: Z97992; PIDN: CAB10796.1; GSPDB: GN00067; SPDB: SPBC30D10.01
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R;Ollver, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G. submitted to the EMBL Data Library, March 1998
A;Reference number: Z21869
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A; Residues: 1-124 <OLI>
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C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000
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A; Introns: 159/1; 272/1; 434/2; 477/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               zuotin-like
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                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-550 <MIL>
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2 rattus norv
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9 homo sapien
1 serratia ma
9 ovis aries
9 schizosacch
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0 pyrococcus
6 drosophila
0 neurospora
0 thermoplasm
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4 mus musculu
4 homo sapien
3 homo sapien
9 arabidopsis
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7 caenorhabdi
9 pseudomonas
4 aspergillus
5 zea mays (m
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9 thermotoga
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1 escherichia
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9 moorella th
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666	621	534	504	454	386	291	264	259	375	375	1151	
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Q9z183 mus muscul	Q92403 agaricus bi	P34610 caenorhabd	P18487 drosophila	P89216 thogoto vi	P37535 bacillus s	P57518 buchnera a	086038 streptomyce	P43563 saccharomy	P70564 rattus norv	P70124 mus muscul	083273 treponema	

ALIGNMENTS

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                                                                                                                                                                  EMBL;
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"Structural studies of receptor binding by
Protein Sci. 6:1516-1528(1997).
Protein Sci. 6:1516-1528(1997).
FUNCTION: THE BETA CHAIN AGGREGATE (B
BINDING TO CELL MEMBRANES.
-i- SUBUNIT: CONTAINS 3 KINDS OF CHAINS. A
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Fraser C.
                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   choleragenoid.
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Maulik P.R., Reed R.A., Shipley G.G.;
"The 2.4 A crystal structure of cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTR MEDLINE=94272319; PubMed=8003954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-78005537; PubMed-903363;
Kurosky A., Markel D.E., Peterson J.W.
"Covalent structure of the beta chain
J. Biol. Chem. 252:7257-7264(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "DNA sequence cholerae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95387394; PubMed=7658472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pentasaccharide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=78005536;
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                                                                                                                                                                                                                                                                                                 (FROM THE SAME PRECURSOR MOLECULE), DISULFIDE BOND, ASSOCIATE NOMEON.
                                                                                                  A01819; XVVCB.
A01810; A05130; A05130
                                                                                                                     X00171; CAA24996.1; -.

K01170; AAA27573.1; -.

D30053; BAA06291.1; -.

X58786; CAA41593.1; -.

X76390; CAA53973.1; -.

X76391; CAA53976.1; -.

X76391; CAA53976.1; -.

AE004224; AAF94613.1; -.
                                 S14624;
2CHB; 03
3CHB; 12
1CHP; 08
1CHQ; 08
1FGB; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.A., Sarfaty S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .M.;
           14; S14624.
03-DEC-97.
12-AUG-98.
08-MAR-96.
08-MAR-96.
23-DEC-96.
01-APR-97.
01-AUG-96.
                                                                                                  A05130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3:166-175(1994).
                                                                                                                                                                                                                                                                                                                                                                                                  Sarfaty S., Jobling M.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         251:550-562(1995).
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                                                                                                                                                                                                                                                                                                            NS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA PRECURSOR MOLECULE), LINKED BY AN INTERCHANASSOCIATE NONCOVALENTLY WITH AN AGGREGATE
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RESULT 2
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Best Local
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STRAND
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STRAND
                                                               Leong J., Vinal A.C., Dallas W.S.; "Nucleotide sequence comparison between cistrons from Escherichia coli of human
                                                                                   SEQUENCE FROM N.A.
STRAIN-ISOLATE H74-114;
MEDLINE-85156481; PubMed-3884513;
                                                                                                                       Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Heat-labile enterotoxin B chain precur
    Yamamoto T., Tamura T.A., Yokota T., T
"Overlapping genes in the heat-labile
from Escherichia coli human strain.";
Mol. Gen. Genet. 188:356-359(1982).
                              STRAIN-ISOLATE H10407;
MEDLINE-83114628; PubMed-6759877;
                                                    Infect.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00772; E ProDom; PD012805;
                                             SEQUENCE FROM N.A.
                                                                                                             Escherichia.
NCBI_TaxID=562;
                                                                                                                                          ELTS OR LTPS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Membrane;
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Pfam; PF01376; Enterotoxin_B; 1.
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R; VC1456;
                                                                                                                                                                                                                 VEVPGSQHIDSQ
                                                         Immun.
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oxin; Signal; 3D-structure; Complete proteome
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Pred.
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No.
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                                                                heat-labile and porcine
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REF.
REF.
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origin.";
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RESULT 3
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Best Local
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EMBL; JO1646; AAB02982.1; -.
EMBL; S60731; AAC60441.1; -.
EMBL; X83966; CAA58800.1; -.
EMBL; X83966; CAA58800.1; -.
PDB; 1LT%; 23-MAR-99.
InterPro; IPRO01835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae.";

Mol. Microbiol. 15:1165-1167(1995).
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                                                                                                                                                                                                                                                                                                                                               DISULFID
VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matkovic-Callogovic D., Loregian A., D'Acunto M.R., Matkovic-Callogovic D., Loregian A., D'Acunto M.R., Tossi A., Palu G., Zanotti G.; "Crystal structure of the B subunit of Escherichia enterotoxin carrying peptides with anti-herpes simple content of the content of the content of the B subunit of Escherichia enterotoxin carrying peptides with anti-herpes simple content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the co
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-I- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.

-I- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISCUSSION OF SEQUENCE MEDLINE=95349400; PubM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Germani Y., Desperrier J.M.;
Submitted (OCT-1996) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-ISOLATE H10407;
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                                                                                                                                           1 VEVPGSQHIDSQ
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12; Conser
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34
    STANDARD;
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124
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1 -> Y (IN ISOLATE |

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να. No. 6e-05;
Mismatches
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H10407).
H10407).
CRC64;
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DISCUSSION OF SEQUENCE.

DISCUSSION OF SEQUENCE.

MEDLING-95349400; PubMed-7623669;

MEDLING-95349400; PubMed-7623669;

MEDLING-95349400; PubMed-7623669;

MEDLING-95349400; PubMed-7623669;

MEDLING-95349400; PubMed-7623669;

MEDLING-95349400; PubMed-7623669;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed R.K., Rappuoli F.MEDLING-9534940;

MEDLING-95349400; PubMed R.K., Rappuoli F.MEDLING-9534940;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed-762369;

MEDLING-95349400; PubMed-762369;

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MEDLLNE=91238966; PubMed=2034287;
Sixma T.K., Pronk S.E., Kalk K.H., Wartna
Witholt B., Hol W.G.J.;
"Crystal structure of a cholera toxin-rela
from E. coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ibrahimi I., Gentz R.;
"A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJURE 85156481; PubMed=3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
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21-JUL-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Teat-labile enterotoxin B chain precursor (LT
                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J.; "Refined structure of Escherichia coli heat-labile enterotoxin, close relative of cholera toxin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS)
MEDLINE-93240541; PubMed-8478941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants
Escherichia coli and Vibrio cholerae Ol.";
J. Bacteriol. 169:1352-1357(1987).
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MEDLINE=87137303; PubMed=3546273;
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MEDLINE-81074965; Pu
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                       SWISS-PROT entry is copyright. It is producen the Swiss Institute of Bioinformatics
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01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Carbon monoxide dehydrogenase beta subunit (EC 1.2.99.2) (CODH).
Moorella thermoacetica (Clostridium thermoaceticum).
Bacteria; Firmicutes; Bacillus/Clostridium group; Moorella group.
                              Morton T.A., Runquist J.A., Wood H.G., Ljungdahl L.G.; "The primary structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the structure of the struct
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17-AUG-96.
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16-JUN-97.
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                                              Voet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert "The sequence of a nearly unclonable 22.8 kb segment on the left a chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A, TIPI, MRF1 genes and six new open reading frames.";
Yeast 13:177-182(1997).
-i- CATALYTIC ACTIVITY: 5-0-(1-carboxyvinyl)-3-phosphoshikimate "
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                                                                                                                                                                                                MEDLINE-3411, ..., Recussor U., Braus G.H.;
Jones D.G.L., Reusser U., Braus G.H.;
"Molecular cloning, characterization and analysis of the regulat."
"Molecular cloning, characterization and analysis of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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MEDLINE=97197983; PubMed=9046099;
Voet M., Defoor E., Verhasselt P.,
                                                                                                                                                                           Mol.
                                                                                                                                                                                       of the ARO2 gene, cerevisiae.";
                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccisaccharomycetales; Saccharomycetaceae; Saccharomyces
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            chorismate + phosphate.
COFACTOR: REDUCED FLAVIN.
PATHWAY: SEVENTH STEP IN
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COFACTOR: NICKEL.
SUBUNIT: TETRAMER OF TWO ALPHA
SIMILARITY: TO R.RUBRUM CARBON
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FUNCTION: CATALYZES THE INTERCONVERSION
SYNTHESIS OF ACETYL-COENZYME A FROM THE
SULFUR PROTEIN, CO, AND COENZYME A.
CATALYTIC ACTIVITY: CO + H(2)O + accepto
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IRON-SULFUR (BY SIMILARITY).
24 MW; 54BA3D816C25F9FC CRC64;
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the Euro
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MEDLINE-9928/316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Prakt M.S., Philips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from
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proDom; PD002941; Chorismate_synt; 1.
pROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
pROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
pROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.
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Bacteria; Thermotogales;
NCBI_TaxID=2336;
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                                                                                                                                                                                                                               Unpublished observations (APR-2001).
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P58009;
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SEQUENCE 376 AA; 40838 MW; AF3AF65605B91E8E
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L; X99960; CAA68214.1;
L; Z72670; CAA96860.1;
; S17246; S17246.
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INDUCTION: BY AMINO ACID STARVATION.
SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
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01-NOV-1995
16-OCT-2001
                                                                                                                      Lyase; Co
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"Determination of a 21548 bp nucleotide sequence around the 24 degrees region of the Bacillus subtilis chromosome.";
Microbiology 141:269-275(1995).
-!- FUNCTION: CATALYZES THE DEHYDRATION OF GLUCARATE TO 5-KETO-4-DEOXY-D-GLUCARATE (5-KDGLUC) (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: D-glucarate = 5-dehydro-4-deoxy-D-glucara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE001773; -: NOT_ANNOTATED_CDS.
TIGR; TM1158.1; -.
Hypothetical protein; Complete protec
SEQUENCE 240 AA; 27773 MW; 1BEF66
                                                                                                                                                                                                  EMBL; D30808; BAA06470.1; -. EMBL; Z99105; CAB12043.1; -. HSSP; P42206; 1BQG.
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                              Pfam; PF01188; MR_MLE; 1. Pfam; PF02746; MR_MLE_N; 1.
                                                                                                                                                                         SubtiList; BG11161; gudD. InterPro; IPR001354; MR_M
                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS
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                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE MANDELATE RACEMA LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VPGSEHLEGK 235
EVPGGEHI 71
                           EVPGSQHI
                                                                                                                     Complete proteome
CE 455 AA; 5078
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5; Conser
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(Rel.
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. 32, Last sequence. 40, Last annotation.
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27773 MW; 1BEF66C1C8BD2700 CRC64
                                                                                                                      50782 MW;
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus/Clostridium group; us group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                 IN GLUCARATE CATABOLISM
TO THE MANDELATE RACEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
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Pred. No. 13;
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Matches 6
NCBI_Ta...
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-99303581; PubMed=1...
Lin C.Y., Anders J., Johnson M.
Calecular cloning of cDNA for
with trypsin-like ac
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09Y5Y6; 09H3S0; Q9HCA3; Q9HB36;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-type serine protease 1) (MT-ST) (Prostamin) (Serine protease TADG-15;
(Tumor associated differentially-expressed gene-15 protein).

ST14 OR PRSS14 OR SNC19 OR TADG15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content institutions.
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-:- CATALYTIC ACTIVITY: Hydrolysis of terminal, non-reducir
galactose residues in beta-D-galactosides.
-:- SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermoanaerobacter ethanolicus (Clostridium thermohydrosulfuricum)
Bacteria; Firmicutes; Bacillus/Clostridium group;
Thermoanaerobacter group; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001649; Glyco_hydro_2.
Pfam; PF00703; Glyco_hydro_2; 1.
Pfam; PF02836; Glyco_hydro_2_C; 1.
Pfam; PF02837; Glyco_hydro_2_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; Y08557; CAA69850.1;
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388 388
453 453
743 AA; 85796 P
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                                                                                                                                                                       PubMed=10373424;
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                                                                                                                                                                                                                                                                                                                                    Chordata;
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54.5%;
                                                                    son M., Sang Q.A., A for matriptase, e activity.";
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Pred.
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NUCLEOPHILE (BY SIMILARITY).
: FE011FF517E51DFC CRC64;
                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae
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                                                                                                                                     Dickson R.B.;
                                                                                                   matrix-degrading
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EMBL; AF11824; AAD42765.2; --
EMBL; AF13086; AAF00109.1; --
EMBL; AB030036; BAB20376.1; --
EMBL; AB030036; BAB20376.1; --
EMBL; BC057145; AAG15395.1; --
EMBL; BC005826; AAG13349.1; --
EMBL; BC005826; AAG13349.1; --
EMBL; BC00763; IDPO.
MEROPS; S01.302; --
InterPro; IPR0001314; Chymotrypsin.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR0012172; LDL_recept_A.
InterPro; IPR001272; LDL_recept_A.
InterPro; IPR001274; Trypsin.
Pfam; PF000431; CUB; 2
Pfam; PF00057; Idl_recept_a; 4.
Pfam; PF00059; trypsin; 1.
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=99432178; PubMed=10500122;
Takeuchi T., Shuman M.A., Craik C.S.;
Takeuchi T., Shuman M.A., Craik C.S.;
"Reverse biochemistry: Use of macromolecular protease inhibitors dissect complex biological processes and identify a membrane-type carrine protease in epithelial cancer and normal tissue.";
carrine protease in epithelial cancer and normal tissue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol.
[2]
                                                                                                                                                                                                                                                      modified
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or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 340-664 FROM Cao J., Fan W., Zheng S. "Genomic analysis of a no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O'Brien T
                                                                                                                                                                                                                                                                                              between
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Yamaguchi N., Mitsui
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European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type II membrane SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLE SIMILARITY: CONTAINS 2 CUB DOMAINS. SIMILARITY: BELONGS TO PEPTIDASE FAMILY TRYPSIN FAMILY.
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                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright.
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SMART; SMART; SMART;

SM00042; SM00192;

CUB; 2 LDLRECEPTOR.

PRINTS;

PR00261;

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RESULT 10
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SMART; SM00192; Tryp_SPc; 1.

PROSITE; PS01109; LDLRA_1; 2.

PROSITE; PS01209; LDLRA_2; 4.

PROSITE; PS50068; LDLRA_2; 4.

PROSITE; PS50040; TRYPSIN_HIS; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Signal-anchor; Glycoprotein; Hyd
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CARBOHYD
CARBOHYD
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YMR306W OR YM9952.08.
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SEQUENCE
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ACT_SITE
                                                                           STRAIN=S288C / AB972:
Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

-i- CATALYTIC ACTIVITY: UDP-glucose + {(1,3)-beta-D-glucosyl}(N)
+ {(1,3)-beta-D-glucosyl}(N+1).

-i- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-i- SIMILARITY: STRONG, TO GLS1 AND GLS2.
                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Saccharomycetaceae; SaccharomycBI_TaxID=4932;
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              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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Judy Leyuence of the plasmid-encoded catechol 1,2-dioxygenase-expressing gene, pheb, of phenol-degrading Pseudomonas sp. strain EST1001.";

RL Gene 98:15-20(1991).

CC -1- COFACTOR: FERRIC ION.

CC -1- COFACTOR: FERRIC ION.

CC -1- PATHWAY: PHENOL DEGRADATION.

CC -1- SIMILARITY: BELONGS TO THE TAMILY.
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PHEB_PSESP
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Bacteria, Proteobacteria.
NCBI_TaxID=306;
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email to license@isb-sib.ch).

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RESULT 13
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SEQUENCE 31
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-!- SIMILARITY: SOME, TO YEAST YDL087C AND S.POMBE SPCC16A11.13.
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Rhabditidae; Peloderinae;
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TE; PS00083; INTRADIOL_DIOXYGENAS; 1.
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C STRAIN=ATCC 15692 / PAO1;

C STRAIN=ATCC 15692 / PAO1;

X MEDLINE=20437337; PubMed=10984043;

A Stover C.K. Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warrener A. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagro A. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan A. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R. A. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., A. Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;

Tomplete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964(2000).

C -1- SIMILARITY: TO E.COLI YCJY.
                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                 TYRO_ASPOR
Q00234;
15-JUL-1998
15-JUL-1998
30-MAY-2000
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;

Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
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NCBI_TaxID=5062;
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aeruginosa.";
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Bacteria; Proteobacteria;
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P49175;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                      THIOETH
SEQUENCE
STRAIN=CV. B73;
MEDLINE=95357417; PubMed=7630946;
Xu J., Pemberton G.H., Almira E.C
                                                                         Spermatophyta; Magnoliophyta; L. Panicoideae; Andropogoneae; Zea
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Eukaryota; Viridiplantae; Streptophyta;
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InterPro; IPR002227; Tyrosinase.
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-!- FUNCTION: THIS IS A COPPER-CONTAINING OF PIGMENTS SUCH AS MELA
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STRAIN-ATCC 22788 /
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SIMILARITY: BELONGS TO THE TYROSINASE FAMILY.
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Pfam; PF00251; Glyco_hydro_32; 1.
PROSITE; PS00609; GLYCOSYL_HYDROL_F32;
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-!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES
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Copyright (c) 1993 - 2000 Comp
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Q9R646;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microbiol. Immunol. 39:87-94(1995).
HSSP; P01556; IXTC.
InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
ProDom; PD012805; Enterotoxin_B; 1.
ProDom; PD012805; Enterotoxin_B; 1.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
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Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
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                   InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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Shin H.J., Park Y.C.,
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                                                          Komase K.;
Submitted
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                   SEQUENCE FROM N.A
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                                                                                                  STRAIN=1032
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Escherichia coll.
Parteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; NCBI_TaxID-666;
                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001835; Enterotoxin_B.
pfam; PF01376; Enterotoxin_B; 1.
PRIMTS; PR00772; ENTEROTOXINB.
ProDom; PD012805; Enterotoxin_B; 1.
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Best Local S
Matches 12
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Q94M01;
01-DEC-2001('
01-DEC-2001('
01-DEC-2001('
CTXB.
CTXB.
Vibrio phage'
                                                                                                                                                                                                                                                                                                                         Q9NKD5;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 43.6 KDA PROTEIN.
BG:DS01514.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; ssDNA viruses; NCBI_TaxID=141904;
           SEQUENCE FROM N.A.
STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.
Doyle C., Galle R., George R., Harris N.,
                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Eukaryota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

Bhattacharyyaa T., Nandy R.K., Nair G.B.;

Bhattacharyyaa T., Nandy R.K., Nair G.B.;

"The entire core region of the ctx-phi (ctx-prophage) in environmental strain of V. cholerae.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF414369; AAA109682.1;

SEQUENCE 124 AA; 13884 MW; 8D4C251591B16891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine 12:1083-1089(1994).
EMBL; AB011677; BAA25726.1; -.
SEQUENCE 124 AA; 14028 MW;
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a trace amount of
vaccine.":
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Tamura S., Asanuma H., Tomita T., Komase K.,
Hattori N., Watanabe K., Suzuki Y., Nagamine
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Conservative
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Last annotation update)
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Pred. No. 0.0
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Pred. No.
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                 .E., Blazej
Hartzell G
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T., Aizawa C.,
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J R., L.
G., Harvey
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CC Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Celniker S.E., Agbayani A., Chavez C., Chew M., Clesiolka L., Doyle C.M.,
CAR Butenhoff C., Champe M., Chavez C., Chew M., Clesiolka L., Doyle C.M.,
CAR Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
CAR Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
CAR Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
CAR Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Caran L.L., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Caran L.L., Rubin G.M.;
Caran L.L., Rubin G.M.;
Caran L.L., Rubin G.M.;
Caran L.L., Rubin G.M.;
Caran L.L., Rubin G.M.;
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Q94HM6;
Q94HM6;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Saaki C., Henry D., Oates R., Simmon.
"Rice Genomic Sequence.",
"Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; AC090873; AAK98653.1; -
EMBL; AC090873; AAK98653.1; -
EMBL; AC090873; AAK98653.1; -
EMBL; AC090873; AAK98653.1; -
EMBL; AC090873; AAK98653.1; -
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EMBL; AC0908745; AAK98653.1; -
EMBL; AC090875; AAK98653.1; -
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Oryza sativa (Rice).
Cukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
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01-DEC-2001 (TremBLrel. 19, Last seque)
01-DEC-2001 (TremBLrel. 19, Last annot;
01-DEC-2001 (TremBLrel. 19, Last annot;
01-DEC-2001 (TremBLrel. 19, Last annot;
01-DEC-2001 (TremBLrel. 19, Created)
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"An exploration of the sequence of a 2.9-mb Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
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zzolo M., Reese M.G., Spradling A., Tsang G., Wan K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CN BW SP;
   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     12
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72.78;
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77.88;
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Pred. No. 4.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 42;
Pred. No.
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                                                                                                                                       1109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
                                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 802;
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Moshrefi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Η.,
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Best I
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01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
0002B05.25 PROTEIN.
P0002B05.25.
                    Submitted
EMBL; APOC
                                                          Sasaki T., Matsumoto T., Yamar
"Oryza sativa nipponbare(GA3)
clone:P0002B05.";
                                                                                                                                                                                                    Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                    Q94EB4;
Q94EB4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-NIPPONBARE;
Spiegel L., de la Bastide
Preston R., Vil M.D., Bake
                                                                                                  STRAIN-CV.
Sasaki T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (AUG-2001)
EMBL; AC078944; AAK93
SEQUENCE 1109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Santos L., Miller B
Shah R., Bahret A.,
McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-NIPPONBARE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller B., Kuit K., Rodriguez S., Cunnius D.M., Balija V., Sl
Bahret A., Bal H., O'Shaughnessy A., Dedhia N., McCombie W.R.
"Genomic Sequence for Oryza sativa, Niponbare strain, clone
OSJNBa0089D15, from Chromosome 10, complete sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                            SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                King
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCombie W.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PGSQHIDSQ 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       er L.E., Spiegel L., de la
L., Preston R., Vil M.D.,
os L., Miller B., Kuit K.,
  tted (JAN-2001)
AP003141; BAB63
NCE 1352 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conserv
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tiva (Rice).
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                                                                                                  NIPPONBARE;
Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
-2001) to the |
| BAB63505.1;
| AA; 154782 |
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77.8%;
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Baker J.,
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                                                                                                    Yamamoto
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Pred. No. 21;
2; Mismatches
    W.
                                       EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                       Last annotation update)
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                                                                           moto K.;
genomic
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., Bell M.,
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Baker J., Be
Rodriguez S.
                                                                                                                                                                                                                                                                                                                                            sequence update)
  DFF265A2B971B8F8 CRC64;
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                                                                               DNA,
                                                                                                                                                                                                                       Embryophyta;
a; Poales; Po
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Bell M., Zuta
S., Cunnius D
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Zutavern
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                                                                               chromosome
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avern T., San
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                                                                                                                                                                                                                         Poaceae;
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HYPOTHETICAL
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the 8 M
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Submitted (
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"Rice Genomic Sequence.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ
EMBL; AC079852; AAL25171.1; -.
SEQUENCE 2535 AA; 289895 MW; DD280569D1541
                   MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapa Kinashi H., Hopwood D.A.; and a d "A set of ordered cosmids and a d
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Oryza sativa (Rice).
Eukaryota, Viridiplantae,
                                                                                                                                                    Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                     SC2A11.21C.
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Ehrhartoideae; Oryzeae; Oryza
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01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
pUTATIVE TNP-LIKE TRANSPOSABLE ELEMENT.
                                                                                               STRAIN-A3(2
                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                     Parkhill
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                                                                                                                                                                         J.,
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(AUG-1998)
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(AUG-1998)
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1 26.0 KDA PR
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77.8%;
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PROTEIN.
 coelicolor
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R., Simmons
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yta; Liliopsida;
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e EMBL/GenBank/DDBJ
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Streptomyces.
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SQ PR PR

InterPro; IPR002502; Amidase_2.
Pfam; PF01510; Amidase_2; 1.
Hypothetical protein.
SEQUENCE 242 AA; 26018 MW;

6DD10FF18A2EC544 CRC64;

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Mol. microbiol. 21:77-96(1996). EMBL; AL031184; CAA20190.1; -.

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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
11-OCT-2000 (TrEMBLrel. 15, Last annotation update)
1LPL, LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENT).
Homo sapiens (Human).
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                                                                   SEQUENCE
Pluvinet
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MEDLINE-99231848; PubMed-10217496;
Okstad O.A., Hegna I., Lindbaeck T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1396;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ATP-DEPENDENT NUCLEASE SUBUNIT A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Microbiology 145:621-631(1999).
EMBL; Y11217; CAA72103.1; -.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
  SEQUENCE FROM N.A
                                              Submitted
                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                     90AN6
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Similarity 58.3%;
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R., Estivill X.,
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                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for inte
human gene transcripts.";
Submitted (JUL-2000) to the EMBL/GenBar
EMBL; AL389957; CAB97531.1; -
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Cerdeno A.M., Parkhill
Submitted (NOV-1999) to
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Oliver K., Harris D.;
Submitted (NOV-1999) to
                                                                                                                                                                                                                                   Redenbach M., Kieser H.M., Denapaite D., Eichner P. Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL; ALI33210; C.M861584.1; -
InterPro; IPR002502; Amidase_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
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29: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
20: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
21: \SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1999.DAT: *
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Gapop 10.0 ,
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Maximum Match 100%
Listing first 45 summaries
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106
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                   he number of results predicted by chance to have a than or equal to the score of the result being printed, by analysis of the total score distribution.
                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3, 2002, 08:54:57; search time 94.52 seconds (without alignments) 24.678 Million cell updates/sec
    DВ
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    17
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  AAY87462
AAW04857
AAR94939
AAW06606
AAW06607
AAW80808
AAB62367
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AAB62367
AAB62367
AAB62370
AAB62370
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                                                                                                                                                                                                                                                                                                              SUMMARIES
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                                    Heat labile entero
Cholera toxin B su
Cholera toxin B su
Cholera toxin B su
Amino acid sequenc
V. cholera cholera
V. cholera cholera
V. cholera cholera
                                                                                                                                                                                                                                               Description
                                                                                                                                                                                     Cholera toxin B/en Synthetic cholera
Cholera Toxin B-su
E. coli LTB protei
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106 100.0 106 100.0 106 100.0 106 100.0 106 100.0 107 109.0 109.3 101 95.3 101 95.3 101 95.3 101 95.3 101 95.3 101 95.3 101 95.3 101 95.3 101 95.3 101 95.3	100. 100. 100. 100. 100. 100.
130 130 1380 2380 2380 2405 103 25 26 27 27 28 29 30 20 20 20 20 20 20 20 20 20 20 20 20 20	
11 ARRO4825 11 AARCH825 12 AAW94082 22 AAU00507 22 AAU00506 14 AAF50340 21 AAF72545 20 AAW95226 21 AAY61816 20 AAW95226 21 AAY68365 21 AAY68365 21 AAF62379 22 AAB62377 23 AAB62373 24 AAB62373 25 AAB62373 26 AAB73244 27 AAB73244 28 AAB73244 29 AAB73244 20 AAB73244 20 AAB73244	0 AAP93561 7 AAW06605 9 AAW99770 9 AAY96652 2 AAG65992 2 AAB62359 2 AAB62363 2 AAB62376 2 AAB62376
rB-CTB fusion pr TB-CTB fusion pr TB-CTB fusion pr TB-CTB fusion pr Coli heat-labi Sv-1 antigen/hea quence of sub-un . coli heat labi DP-ribosylating scherichia coli . coli heat-labi eat labile toxin coli verotoxin- coli roperote . coli LTB prote . ubunit of the h Cholera toxin B su Amino acid sequenc Plant-optimized E. Cholera toxin B su V. cholera strain V. cholera cholera V. cholera cholera E. coli LTB protei E. coli LTB protei	

ALIGNMENTS

RESULT AAY87462

Cholera toxin B/enterotoxin B-derived peptide,

SEQ ID NO:4

EtxB;

03-JUL-2000 (first entry)

AAY87462;

AAY87462 standard; peptide;

21 ΑA

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Vibrio cholerae.
Escherichia coli.
                                                                                                                                                           Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                         Williams NA, Hirst TR;
                                                        (UYBR-) UNIV BRISTOL.
                                                                       07-SEP-1998;
                                                                                     07-SEP-1999;
                                                                                                    16-MAR-2000
                                                                                                                 WO200014114-A1
                                                                                                                                                      adjuvant; immune
                            2000-256943/22.
                                                                       98GB-0019484.
                                                                                      99WO-GB02970
                                                                                                                                                     disorder; diarrhoea.
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Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

the

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous

Disclosure; Page 15;

62pp; English.

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AAW04857
ID AAWC
QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative (
                                                                               Recombinant constructs for expressing and opt. secreting proteins in Bordetella - comprise Bordetella promoter coupled to non-Bordetella, esp. cholera B toxin, gene or coupled to non-Bordetella leader and
                             gene of interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural protein; receptor; heterologous gene; leader; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bordetella pertussis; whooping cough; recombinant construct; cholera toxin B subunit; enzyme; antigen; immunogen; allergen; enzyme inhibitor; hormone; lymphokine; immunoglobulin; toxin;
                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                             Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW04857;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-FEB-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CONN-) CONNAUGHT LAB LTD
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                                                                                                                                                                                                                                                                                  AAT38038
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                                                                                                                                                                                                                                                                                                                                                                                                                             Loosmore SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-CA00107
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                                                                                                                                                                                                                                                                                                                                                                                                                             Yacoob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 5.1e-11;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                             RK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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24-OCT-1994; 24-OCT-1995;

94US-0328716 95WO-US13376

A transgenic plant comprising or expressing a DNA sequence encoding an immunogenic agent can be be used as an oral vaccine for animals. The vaccine is administered by the oral consumption of the plant and

Transgenic plants contg.

as oral vaccines

for animals

consume

enterotoxin subunits ume the plant

E. coli heat labile

WPI; 1996-230602/23. N-PSDB; AAT18799, AAT18800

Arntzen CJ,

Clements

'n,

Haq

TA,

Mason

;SH

(TULA) TULANE EDUCATIONAL FUND. (TEXA) UNIV TEXAS A & M SYSTEM.

Disclosure;

Page 100-101; 130pp;

English which

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fragments, toxins, mammalian proteins, structural proteins or receptors. The Bordetella strains are particularly engineered to express the cholera toxin B subunit (this sequence). The promoters used in the constructs are selected from the Bordetella pertussis tox, fha promoters or the high molecular weight (hnw) outer membrane promoter of non typable Haemophilus influenzae; leaders used in the constructs are selected from the cholera toxin B leader (CTB-L), the pertussis toxin subunit SI leader (SI-L) and the pertussin pertactin leader (PN-L); and genes used in the constructs are selected from a novel synthetic cholera toxin B gene (ctb) and the hmw1 and hmw2 genes of Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                    Recombinant constructs comprising a promoter functional in Bordetella operatively linked to a heterologous gene or a non-Bordetella leader sequence for secretion of a gene product which may or may not be of Bordetella origin, can be used for the expression in Bordetella of enzymes, antigens, immunogens, allergens, enzyme inhibitors, hormones, lymphokines, immunoglobulins or their
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Figure 1; 61pp;
     103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               English
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AAR94939
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                     adjuvant;
                                                                                                                                                                                           AAR94939;
                                                           Escherichia coli.
                                                                                                                                Heat labile enterotoxin B subunit (LT-B) E.coli.
                                                                                                                                                              31-OCT-1996 (first entry)
                                                                                                                                                                                                                       AAR94939 standard;
02-MAY-1996
                              WO9612801-A1
                                                                                                    Toxin; subunit; vaccine;
                                                                                                                                                                                                                                                                                              45
                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                           1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                    ω
                                                                                                                                                                                                                                                                                             gatfqvevpgsqhidsqkkai 65
                                                                                       immunisation.
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                        Protein; 103
                                                                                                    transgenic plant; immunogen; antigen;
                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 17;
Pred. No. 3.2e-10;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                        Gaps
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δÃ В

100.0%;

Length

103;

0,

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RESULT
AAW06606
ID AAW0
  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using transgenic plants, where the plants express bacterial antigens that act as both immunogens and adjuvants. The method provides an inexpensive production and delivery system for such antigens to animals. This is the LT-B Escherichia coli toxin subunit and its coding sequence was used in the construction of such a transgenic plant. The immunogenic agent preferably comprises the LT-B or CT-B (cholera toxin B subunit) or optionally LT-A or CT-A.
                                                                                                                                                                                                                                                                                          Chimeric - Vibrio cholerae.
Chimeric - Enterotoxigenic
 AAW06606 is enterotoxin
                         Claim 3;
                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                         06-AUG-1997
                                       Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                              (HOLM/)
                                                                                                                                       05-MAY-1995;
                                                                                                                                                                     07-NOV-1996
                                                                                                                                                                                    W09634893-A1
                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                        Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                                                                                                                                                                                                                                                         AAW06606;
                                                                                                                                                                                                                                                                                                                                                                                                        AAW06606 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                               Holmgren J,
                                                                                                                                                      02-MAY-1996;
                                                                                                                                                                                                                                                                                                                 vomiting;
                                                                                                                                                                                                                                                                                                                                 heat
                                                                                                                                                                                                                                                                                                                        immunogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                               45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                       4
                                                                        1996-506108/50.
DB; AAT43576.
                                                                                                                                                                                                                                                                                                                       labile enterotoxin B subunit; LTB; vaccine; nogen; antigen; broad spectrum; cross reacti
                                                                                                                                                                                                                                                                                                                                        labile;
                                                                                                                                                                                                                                                                                                                                                                                                                                             gatfqvevpgsqhidsqkkai 65
                                                                                                              HOLMGREN
LEBENS M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                        Page -;
                                                                                                                                                                                                                                                                                                                food poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                                                         Enterotoxigenic Escherichia
 BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                        tolerant; stable; hybrid; cholera toxin B subunit; CTB;
                                                                                               Lebens
                                                                                                                                                                                                                                                                                                                                                                        (first
mature cholera toxin B subunit (CTB)/heat
subunit (LTB) hybrid molecule. In mature C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA;
                                                                                                                                       95SE-0001682
                                                                                                                                                      96WO-SE00570
                                                                                                                                                                                                                                           /note=
94
                                                                                                                                                                                                                   /note=
95
                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                               ₽.4
                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                    'label=
                                                                                                                                                                                                                                                           'label=
                                                                                                                                                                                                            label=
                                                                                                                                                                                                                                                                                                                                                                                                       Protein;
                                                                                               MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%;
                         English
                                                                                                                                                                                                   "wild-type Ala
                                                                                                                                                                                                                                                  "wild-type Thr
                                                                                                                                                                                                                          "wild-type
                                                                                                                                                                                                                         substitution
"wild-type His
                                                                                                                                                                                                           substitution
                                                                                                                                                                                                                                                           substitution
                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
                                                                                                                                                                                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 106; DB 17;
Pred. No. 3.2e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         cross reactive; diarrhoea;
                                                                                                                                                                                                   replaced
                                                                                                                                                                                                                          replaced
                                                                                                                                                                                                                                                  replaced
                                                                                                                                                                                                                                                                                         Coli
                                                                                                                                                                                                   γd
                                                                                                                                                                                                                           þу
                                                                                                                                                                                                                                                  уd
                                                                                                                                                                                                                                                                                                                                 immunisation
                                                                                                                                                                                                                                                   Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
CTB protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT
AAW06607
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Note - This sequence does not appear in the specification, it is a claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
Chimeric
                                                                                     WPI; 1996-506108/50.
N-PSDB; AAT43577.
Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in vaccines against enterotoxin-induced illness
                                                                                                                                                                                                       (HOLM/)
                                                                                                                                                                                                                                                                                                                      02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat labile; tolerant; stable; hybrid; cholera toxin B subunit; CTB; heat labile enterotoxin B subunit; LTB; vaccine; immunisation; immunogen; antigen; broad spectrum; cross reactive; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin B subunit/heat labile enterotoxin B subunit hybrid.
                                                                                                                                                             Holmgren
                                                                                                                                                                                                                                                                          05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                               07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW06607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW06607 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           WO9634893-A1
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                                                                                                                                                                                                         LEBENS M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 100 21; Conservative
                                                                                                                                                                                                                           HOLMGREN
                                                                                                                                                    ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae
Enterotoxigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 AA;
                                                                                                                                                             Lebens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    poisoning.
                                                                                                                                                                                                                                                                          95SE-0001682
                                                                                                                                                                                                                                                                                                                   96WO-SE00570
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= substitution
/note= "the first 25 amino acids of mature
/note= "the first 25 amino acids of mature
wild-type cholera toxin B subunit are
replaced with the first 25 amino acids
of mature enterotoxin B subunit"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein; 103
                                                                                                                                                               ΜR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6; DB 17;
. 3.2e-10;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Claim 4; Page -;

32pp; English

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RESULT
AAW80808
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Best Local
                   This is the amino acid sequence of the cholera toxin B subunit used the method of the invention involving the use of nontoxic subunits a an effective adjuvant in coadministration of an antigen to birds and animals. In addition to the use of the toxin as an uncosal adjuvant, it also provides a vaccine comprising the toxin, an immunogenic amount of an antigen, and a pharmaceutically acceptable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW06007 is a mature cholera toxin B subunit (CTB)/heat labile enterotoxin B subunit (LTB) hybrid molecule. In mature CTB proteir certain amino acids (aa) were replaced with corresponding aa from heat-labile enterotoxin B subunit (LTB). The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic illness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin induced illness, e.g. diarrhoea
          carrier.
                                                                                                                          Disclosure; Fig 1B; 43pp; English.
                                                                                                                                                                       New mutant cholera toxin selected from subunits/derivatives - effective as an
                                                                                                                                                                                                                                                Kiyono
                                                                                                                                                                                                                                                                                           (TAKE/)
(UABR-)
                                                                                                                                                                                                                                                                                                                                                                     04-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of the wild type chorela toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW80808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW80808 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and vomiting,
                                                                                                                                                                                                                                                                             (YAMA/)
                                                                                                                                                                                                                                                                                                                                      (KIYO/)
                                                                                                                                                                                                                                                                                                                        (MCGH/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nd vomiting, in humans and animals.

ote - This sequence does not appear in the specification, it is claimed mutant sequence of mature cholera toxin B subunit (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 თ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gatfqvevpgsqhidsqkkai 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                               Η,
                                                                                                                                                                                                                                                                          ) KIYONO H.
) MCGHEE J R.
) TAKEDA Y.
) UAB RES FOUND.
) YAMAMOTO S.
                                                                                                                                                          antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
         The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bird;
                                                                                                                                                                                                                                               Mcghee JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
          toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B subunit; nontoxic subunit; adjuvant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   animal; mucosal; vaccine.
                                                                                                                                                                                                                                                                                                                                                                     97US-0043410
                                                                                                                                                                                                                                                                                                                                                                                                98WO-US06725
                                                                                                                                                          to birds
          can be used with single/multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                  Takeda
                                                                                                                                                          and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                         mammals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 106; DB 17;
Pred. No. 3.2e-10;
                                                                                                                                                                                                                                                  Υ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                        adjuvant when coadministered
                                                                                                                                                                                       מ
                                                                                                                                                                                    group comprising nontoxic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coadministration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
          it
                                                                            in as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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vaccines,

Query Match
Best Local Similarity

100.0%;

Score 106; DB 22; Pred. No. 3.2e-10;

Length 103;

Sequence

103

AA;

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SSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches : 21
                           The invention relates to a recombinant AB5B subunit protein comprising at least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a wild type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cysteines to an immunogen or vaccine. Recombinant mutant CTB (TCTB) can be used in the treatment of autoimmune diseases e.g. rheumatoid arthritis, encephalomyelitis (or other neuron demyelinating diseases) and diabetes. The TCTB or other B subunits of the invention can also be used to induce tolerance to infection, e.g. parasitic infection. The present sequence represents a CTB variant protein, NCBI GenBank No. GI 1421511.
                                                                                                                                                                                                                                                                                                  Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                infection; parasitic; immunosuppressive; antiarthritic; antirheumatic;
antidiabetic; neuroprotective; vaccine; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         enables the possibility for commercial mucosal adjuvants for use humans, since these are more effective and safer than vaccines administered subcutaneously.
                                                                                                                                                                                                                                                     Disclosure; Page 67-68;
                                                                                                                                                                                                                                                                                                                                                                                               Handley HH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-OCT-2000; 2000WO-US27607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB5B subunit protein; mutation; recombinant; cholers immunogen; autoimmune disease; neuron demyelinating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V. cholera cholera toxin B (CTB) protein variant (GI 1421511)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB62367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB62367 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                     treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                            (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200127144-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogen;
infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                2001-281974/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Haaparanta T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0158561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                     78pp; English
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                                                                                                                                                                                                                                                                                                                                                                                               Ewalt KL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 106; DB 19;
Pred. No. 3.2e-10;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cholera toxin B; CTB;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB5B subunit protein; mutation; recombinant; cholera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; infection; parasitic; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; neuroprotective; vaccine; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for treating autoimmune diseases -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V. cholera cholera toxin B
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                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                          protein,
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                                                                                                                                                              h 100.0%;
Similarity 100.0%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                        c infection. The present NCBI GenBank No. GI 1421
                                                                                                                                                                                                                                                                  103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                      present sequence represents a CTB variant GI 1421525 (Ogawa 41 R35D).
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Pred. No.
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RESULT
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant AB5B subunit protein comprising a mutation that alters number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AB5B subunit protein; mutation; recombinant; cholera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; infection; parasitic; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; neuroprotective; vaccine; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a recombinant AB5B subunit protein comprising least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a wild type
AAR04163
                                                  AAR04163 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating autoimmune diseases
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                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                 Score 106; DB 22;
Pred. No. 3.3e-10;
Mismatches 0;
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cholera toxin B-subunit; hybrid protein; heterologous IgA active antigen

(first entry)
B-subunit.

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RESULT
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      (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                              E. coli LTB protein variant (GI: 1395122).
                                                                                                                                                                                               AAB62374 standard; Protein;
                                                                                                                                                                                                                                                                                                                             Mature cholera toxin B-subunit is obtained when the signal peptide is cleaved off. There is an Ochre codon at position 343-5; the sequence downstream from it is part of a plasmid.
                                                                                                                                                                                                                                                                                                                                                                                     New hybrid protein, useful in vaccines - contains cholera toxin b subunit and heterologous IgA active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference
                        08-OCT-1999;
                                      05-OCT-2000;
                                                       19-APR-2001
                                                                       WO200127144-A2
                                                                                       Escherichia coli.
                                                                                                                                                                29-JUN-2001
                                                                                                                                                                               AAB62374;
                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                               antigenic sequence.
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ilarity 100.0%;
Conservative
                                       2000WO-US27607
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                                                                                                      neuroprotective;
                        99US-0158561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*label= signal peptide
/*note= absent from mature protein
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                                                                                                                                                                                                                                                                                                                                                               French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE L'ETAT A LIEGE.
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Pred. No. 3.8e-10;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                             The invention relates to a recombinant AB5B subunit protein comprising a least one mutation, where the mutation alters the number of amino acid residues available for chemical modification as compared to a will type AB5B subunit protein, and where the recombinant protein retains an effective target ligand binding affinity. A recombinant AB5B subunit
                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 70; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Handley HH,
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1 GATFQVEVPGSQHIDSQKKAI 21
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haaparanta
                                                                                                                                                       AA,
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                                                        0;
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                                                                      Score 106; DB 2
Pred. No. 4e-10;
                                                        Mismatches
                                                                                          22;
                                                        0;
                                                        Indels
                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                           comprising at amino acid
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                                                      Gaps
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AAP93561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
WPI;
                                                                                                               30-SEP-1988;
                                                                                                                                                                                                                                              Key
Peptide
                                                                                                                                                                                                                                                                                         Escherichia
                                                                                                                                                                                                                                                                                                                                 circumsporozoite protein; fusion protein;
                                                                                                                                                                                                                                                                                                                                              B subunit; heat-labile enterotoxin; LT-B;
                                                                                                                                                                                                                                                                                                                                                                            B subunit of the heat-labile enterotoxin (LT-B) derived from E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAP93561;
                           Brey RN,
                                                                                    02-OCT-1987;
                                                                                                                                            06-APR-1989
                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                    Salmonella; epitope.
                                                                                                                                                                                                                                                                                                                                                                                                          06-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP93561 standard;
                                                       (PRAX-)
                                                                                                                                                                          WO8902924-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 gatfqvevpgsqhidsqkkai 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
 1989-114399/15
                                                       PRAXIS
                           Majarian WR,
                                                                                                                                                                                                                                                                                         coli.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                       BIOLOGICS
                                                                                    87US-0104735
                                                                                                                 88WO-US03376
                                                                                                                                                                                                                                                 Location/Qualifiers
1..22
                                                                                                                                                                                                   /note="Mature LT-B"
                                                                                                                                                                                                                               /note="Signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 124
                            Pillai S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                           Hockmeyer WT;
                                                                                                                                                                                                                                                                                                                                  Escherichia coli; malari live recombinant vaccine;
                                                                                                                                                                                                                                                                                                                                                 malaria;
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RESULT 13
AAW06605
ID AAW0666
XX AAW0666
XX AAW0666
XX Choler
XX Heat 1
KW heat 1
KW immuno
XX Vibrio
XX Vibrio
XX FF Reptid
FT Peptid
FT Peptid
FT Peptid
FT POS-MAY
XX NOS-MAY
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In the patent, the DNA encoding LT-B is expressed as part of a fusion protein with an epitope of a malaria parasite, eg Region I or Region II or a repeat region of circumsporzoite protein antigen (CS) (AAP93560) from Plasmodium berghei. Pref. the fusion gene is inserted into attenuated Salmonella enteriditis under the left promoter control of lambda. Such bacteria can multiply in the host without causing disease disorder and express CS that will induce a protective immune response against malaria and can be used in vaccines. Such vaccines can be
                                      Heat-labile enterotoxin B sub-unit and cholera toxin B sub-unit hybrid protein - opt. fused to immunogenic sequence for use in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Live recombinant vaccine for malaria - comprising attenuated entero-invasive bacterium contg. DNA
                                                                                                                                                                                                                                                                         05-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                         07-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cholera toxin B subunit, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding epitope of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                   Holmgren J,
                                                                                                                                                                                                                                                                                                              02-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                  W09634893-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vomiting;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat labile; tolerant; stable; hybrid; cholera toxin B subunit;
heat labile enterotoxin B subunit; LTB; vaccine; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW06605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW06605 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                           (LEBE/)
                                                                                                                                                                                                                                 (/MIOH)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunogen; antigen; broad spectrum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                      1996-506108/50.
DB; AAT43575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gatfqvevpgsqhidsqkkai
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                                                                                                                                                                                                                                 HOLMGREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                           LEBENS M
                     against enterotoxin-induced illness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3/17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                   Lebens MR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                              96WO-SE00570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         poisoning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA,
                                                                                                                                                                                                                                                                       95SE-0001682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= sig_peptide
22..124
/label= mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                           ₽.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106; DB 10
No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for hybrid immunogenic toxin production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cross reactive; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxin B subunit (CTB), this sequence is described as unpublished in the specification. The mature CTB protein was used to create hybrid mutants, in which certain amno approximation of CTB were replaced with corresponding as from heat-labile enterotoxin B subunit (LTB), see AAW06606 and AAW06607. The specific amino acid substitutions impart LTB-specific epitope characteristics to immunogenic mature CTB. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTB-specific epitope characteristics to immunogenic mature CTB. The hybrid molecules have increased cross-reactivity and are suitable for a broad spectrum vaccine to protect against enterotoxigenic fliness. Immunogenic proteins comprising the hybrid molecules can be used to treat, or in a vaccine to prevent, enterotoxin-induced illness,
                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                               WPI; 1998-297947/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Beta-subunit of heat labile enterotoxin; LTB; fusion protein; vaccine; immunogen; antigen; inhibin; fertility; follicle stimulating hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW59770;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure;
                                                                                                                                                                         enterotoxin
                                                                                                                                                                                                                                                         Bagdasarian
                                                                                                                                                                                                                                                                                                             12-NOV-1996;
                                                                                                                                                                                                                                                                                                                                         12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of E. coli LTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. diarrhoea and vomiting, in humans and animals.
                                                                                                                                                inhibin
                                                                                                                                                                                         New nucleic
                                                                                                                                                                                                                                                                                  (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                                                                                                                                                                                                                    22-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                             WO9821344-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSH; sperm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                          nucleic acid encoding fusion of antigenic peptide and srotoxin sub-unit - useful as vaccinating immunogen, particincreasing animal fertility by inducing antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gatfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV41573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 is the full (including the signal peptide) length cholera subunit (CTB), this sequence is described as unpublished in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ova;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                               96US-0747410
                                                                                                                                                                                                                                                                                                                                        97WO-US20584
                                                                                                                                                                                                                                                         Ireland
                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 106;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4e-10;
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                                                                                                                                                                         particularly
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where the antigenic peptide is an inhibin fragment for increasing the fertility of an animal (by increasing levels of follicle stimulating hormone (FSH) or production of sperm or ova), but more generally for inducing an immune response against the antigenic peptide. Vaccines

This is the amino acid sequence of Escherichia coli beta-subunit of heat labile enteritoxin (LTB). It is used in the method of the invention to create fusion proteins which are useful as vaccinating immunogens. The fusion proteins are useful in vaccines, specifically where the antigenic peptide is an inhibin fragment for increasing the

Disclosure;

Fig 9;

56pp; English.

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RESULT 15
AAY96652
IDY AAY966
XX AAY966
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AC AAY966
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                                              This synthetic Escherichia coli heat-labile toxin (LT) B subunit (LT-B) is encoded by a plant-codon optimized cDNA. The CDNA sequence contains plant-preferred codons and eliminates sequence motifs associated with spurious mRNA processing. The second codon is changed from AAT encoding Asn to GTG encoding Val, in order to create a NCOI restriction site at the 5' end. Novel polynucleotides encode a mutant LT-A polypeptide or a mutant Vibrio cholerae cholera toxin (CT) A subunit (CT-A) polypeptide, which have reduced enzyme activity as compared to the wild-type LT-A or CT-A polypeptide and where at least one of the codons is altered to a plant preferred codon. The polynucleotide further comprises a nucleic acid sequence encoding LT B subunit (LT-B) or a CT B subunit (CT-B). The polynucleotides are useful for the transformation of plant cells for the
                       production of transgenic plants to produce edible vaccines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding LT-A or CT-A polypeptides for the transformation of plant cells, useful in immunogenic composition elicit immune responses in animals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adjuvant; anti-bacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Fig 5A-B; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
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(ARNT/) ARNTZEN C J.
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)B; AAA51156.
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                                 oral vaccines in transgenic plants for the prophylactic or therapeutic treatment against E. coli or V. cholerae. The mutant polypeptides are also useful as adjuvants.
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US-08-952-337-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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PCT-US95-11684-4	US-09-541-782-6	US-08-469-830-11	US-08-416-950-11	US-08-714-070A-1	US-09-564-805-234	5194375-6	US-09-025-580-36	US-09-025-580-35	US-08-602-359A-34	US-08-475-879-94	US-08-485-607-94	US-08-476-537-94	US-07-956-700B-94	US-08-352-902D-133	US-08-961-810-133	US-09-059-461-2	US-08-209-521-30
Sequence 4, Appli	Sequence 6, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 1, Appli	Sequence 234, App	Patent No. 5194375	Sequence 36, Appl	Sequence 35, Appl	Sequence 34, Appl	Sequence 94, Appl	Sequence 94, Appl	Sequence 94, Appl	Sequence 94, Appl	Sequence 133, App	Sequence 133, App	Sequence 2, Appli	Sequence 30, Appl

ALIGNMENTS

Minimum

Maximum

Database

Searched:

Scoring table: Sequence: Perfect score: Title: Run on: OM protein -

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GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: E0T/SE96/00570
EARLIER APPLICATION NUMBER: E0T/SE96/00570
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION. ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER APPLICATION NUMBER: SE 9501682-0
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y Match 100.0%;
Local Similarity 100.0%;
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Pred. No. 2.5e-11;
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US-08-952-337-6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FIRM PC-DOS/MS-DOS
PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEPAX: 416-505-777
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
FILLING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
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      45
                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Stewart, Michael I REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 07-JUN-1995
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M5G 1R7
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                                                                                                                              Conservative
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Pred. No. 2.5e-11;
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                                                                                                                                                                                                                        Patent No.
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                                                                                                                                                                                                           GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                           TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCE: 56 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 01-DEC-199
CLASSIFICATION: 435
                                                                                                                                        APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Klein, M
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palan
                              STREET: 330 Ur
CITY: Toronto
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COUNTRY:
                                                             ADDRESSEE:
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                                             330 University Avenue,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6th Floor,
Canada
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Zealey, Gavin R
Klein, Michel H
                                                                                                                                                                                          Loosmore, Sheena M.
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                             Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 106;
100.0%; Pred. No.
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                                              6th Floor
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-09-013-047-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09374597
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APPLICATION NUMBER: US/
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/
FILING DATE: FEBRUARY 2
                                                                                                        COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/4/2/1/APPLICATION NUMBER: US 08/4/2/1/APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/393,334
                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
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LENGTH: 103 amino acid
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                             CITY: Toronto
STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: UFILING DATE: 23-FEB-1
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M5G 1R7
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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 08/393,334
RY 23, 1995
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                                                                                       US/09/374,597
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Pred. No. 2.5e-11;
Prestrictes 0;
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RESULT 7
US-09-191-852-21
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US-09-191-852-21
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Best Local Similarity
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                     TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-CCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Hag
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
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ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 249
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                 SEQUENCE CHARACTERISTICS
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                                                                                     TELEPHONE: 713-651-5246
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ZIP: 77010
                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
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                  TOPOLOGY:
                                                                                                                                                                           REGISTRATION NUMBER: 40,612
                                                                                                                                                                                              NAME: Fox, David L.
                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                  LENGTH:
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   GY: linear
                                 : 103 amino acids amino acid
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1301 McKinney, Suite 5100
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                  linear
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Pred. No. 2.5e-11;
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Query Match Best Local Similarity

100.0%;

Score 106; DB 4; Pred. No. 2.5e-11;

Length 103;

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US-08-952-337-1
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GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNI
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT APPLICATION NUMBER: PCT/SE96/00570
EARLIER APPLICATION NUMBER: PCT/SE96/00570
                                                                                                                                                                                 Sequence 1, Application US/08952337 Patent No. 6019973
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APPLICATION NUMBER: US 08/328

PRILING DATE: 24 -OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: JONES, JOHN W.

REGISTRATION NUMBER: 31,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
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APPLICANT: 310 Wisenbaker
APPLICANT: COllege Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
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CITY: H
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ZIP: 77027-9095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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1177 West Loop South, 10th Floor
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Pred. No. 2.5
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          2.5e-11;
                                                                                                                                                                                                                                                                                                                                                                                          DB 5;
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                                                                                            SUBUNITS
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RESULT 11
US-08-747-410-2
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SEQ ID NO 2
LENGTH: 123
TYPE: PRT
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                                                                                                                                                           Sequence 2, Application US/08747410
Patent No. 5993820
GENERAL INFORMATION:
APPLICANT: BACDASARIAN, Michael
APPLICANT: IRELAND, James
TITLE OF INVENTION: CHIMERIC LTB VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 123
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Best Local
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: SE 9501682-0 EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Eschcerichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Vibrio cholerae
COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                               NUMBER OF SEQUENCES:
                                                              CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                             65
                                 ZIP:
                                               COUNTRY:
                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                             ADDRESSEE:
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No. 601997.
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                                                                                            E: Merchant, Gould, Smith, Edell, 3100 No. 5993820west Center, 90 St
                                                USA
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Pred. No. 3.1e-11;
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; ORIGINAL SOURCE:
US-08-747-410-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 26,
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acid
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                   APPLICANT: ARMSTROI APPLICANT: HAZES, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kettelberger, Denise M
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 12-NC
                             CLASSIFICATION: 435
                                            FILING DATE:
                                                                                                                                                                ZIP: M5G 1R7
                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                              STATE:
                                                                                                                                                                                                         CITY: Toronto
                                                                                                                                                                                                                          STREET:
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TELEFAX: 612/332-9081
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                                                                                                                                                                                            Ontario
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                                                                                                                                                                                                                       E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 amino acids
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                                                                                                                                                                              Canada
                                                                                                                                                                                                                                                                                                  HAZES, Bart
                                                                                                                                                                                                                                                                                                                              KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                               ARMSTRONG, Glen D.
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100.0%; Pred. No. 3.2e-11;
tive 0; Mismatches 0;
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US 08/110,947
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GENERAL IN
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Best Local :
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 24-AUG-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                             FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
                                                                                                                                                          APPLICATION NUMBER: US 0:
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Suite
CITY: Toronto
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STRANDEDNESS: sir
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REFERENCE/DOCKET NUMBER: 1038-388
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                                                                                                                                                                                                                                               APPLICATION NUMBER:
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o. 5965385
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M5G 1R7
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Similarity 95.2%;
STEWART, Michael I.
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Suite 701, 330 University Avenue
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                                                                                                                                                                               US 08/467,536
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RESULT 14
US-08-467-536-26
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Best Local :
                                                                                                                                                                                                                                                                                                      FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                   TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26
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SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
                                                                                                                                                                      NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE, DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/292,968
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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REFERENCE/FOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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CURRENT APPLICATION DATA:
ADDITORMINATION NUMBER. 16/08/467 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDAGE STREET: SULTER TOYONTO CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL CONTROL 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 0
FILING DATE: 22-AUG-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 06-JUI
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STRANDEDNESS: sir
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M5G 1R7
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5977304
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STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
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Pred. No. 1.7e-10;
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US-08-467-976-26
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Best Local S
Matches 20
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                                                                                               TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO: 1
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                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 31-MAY-1994
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APPLICATION NUMBER: US 08
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: COTTON DOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                           REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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STREET: Sur
STRY: Toronto
                TOPOLOGY:
                              STRANDEDNESS:
                                                                                                                                                                           NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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STRANDEDNESS: si
TOPOLOGY: linear
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les 20; Conserv
                                                              LENGTH:
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                                            amino acid
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                                                                93 amino acids
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                linear
                                                                                                                               (416) 595-1155
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06-JUN-1995
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Pred. No. 1.7e-10;
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Query Match Best Local Similarity

95.3%; 95.2%;

Score 101; DB 3; Pred. No. 1.7e-10;

Length 93;

Matches 20; Conservative 0; Mismatches 1; Indels

0; Gaps 0;

Db Qy

Search completed: July 3, 2002, 08:55:39 Job time: 214 sec

Page 7

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Title:
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length: 2000000000
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18.431 Million cell updates/sec
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106
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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    1 US-09-786-648-4

1 US-08-393-334-2

11 US-08-782-832-15

12 US-08-817-906-21

12 US-09-836-433-20

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Sequence 4, Appli
Sequence 2, Appli
Sequence 15, Appl
Sequence 17, Appl
Sequence 21, Appl
Sequence 20, Appl
Sequence 20, Appl
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Sequence 19, Appl Sequence 37800, A	e 3773,	nce 761, A	58246,	nce 58247,		5824	293	4	2, Ap	419	ω	1,	1,	4,	2	ν	e 2	4, 2	ω	7, 2	e 57,	57,	<u>ب</u>	ი ი	ω, •		equence 26,	10,	5, 2	22,	18,	e 15,	e 2,	'n	Sequence 55,	Sequence 55, Appl

ALIGNMENTS

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US-09-786-648-4

Sequence 4, Application US/09786648

GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: E. coli;
FEATURE:
CONTION: 45...65
OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivabl;
OTHER INFORMATION: human variant E. coli
US-09-786-648-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 4
LENGTH: 21
TYPE: NEW TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOT
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Matches 21; Conserv
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                                                                                                                                                                    Score 106;
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US-08-782-832-15; Sequence 15, Application US/08782832; GENERAL INFORMATION:
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US-08-393-334-2
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GENERAL INFORMATION:
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Best Local :
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                              APPLICANT: Arntzen, Charles J.
APPLICANT: Mason, Hugh S.
APPLICANT: Hag, Tariq A.
APPLICANT: Hag, Tariq A.
TITLE OF INVENTION: PRODUCTION OF AN ORALLY IMMUNOGENIC
TITLE OF INVENTION: BACTERIAL PROTEIN IN TRANSGENIC PLANTS
                                                                            NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOOSMORE, Sheena
APPLICANT: Yaccob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                      STREET:
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Houston: TX
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amino acid
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                                      E: Pravel, Hewitt, Kimball & Krieger 1177 West Loop South, 10th Floor
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US-08-817-906-21; Sequence 21, Applicat: GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
REGISTRATION NUMBER: 33,924
REFERENCE/DOCKET NUMBER: 36170/3
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                                                                   REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements, APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
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MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                   NAME: FOX, David L. REGISTRATION NUMBER: 40,612
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 08/04/97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 1301 McKinney, Suite 5100
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ZIP: 77027-9095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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ative 0;
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; TOPOLOGY:
US-08-817-906-21
                                                                                                                               ; ORGANISM: synthetic construct US-09-836-433-20
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                                                                                                                                                                   SEQ ID NO 20
LENGTH: 116
                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09836433
GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0 SEQ ID NO 14
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Best Local :
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Best Local Similarity
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APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HUBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                         TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE FILE REFERENCE: Not Assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 103
TYPE: PRT
                                                                                                                                                          TYPE: PRT
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                                                                      Local
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LENGTH:
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Pred. No. 1.1e-09;
Mismatches 0;
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Pred. No. 9.8e-10;
; Mismatches 0;
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Pred. No. 9.8e-10;
; Mismatches 0;
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RESULT

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APPLICANT: Mason
APPLICANT: Mason
APPLICANT: Arntzen
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/84454
CURRENT APPLICATION NUMBER: US/09/470,124
CURRENT FILING DATE: 1999-12-24
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia coli
US-09-470-124-55
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SOFTWARE: Patentin Ver. 2:
SEQ ID NO 55
LENGTH: 124
TYPE: PRT
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Sequence 55, Application PC/TUS9930747
GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4860,85427
CURRENT APPLICATION NUMBER: PCT/US99/30747
CURRENT ETLING DATE: 1999-12-22
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PCT-US99-30747-55
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SEQ ID NO 22
LENGTH: 119
TYPE: PRT
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Best Local S
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Best Local Similarity 100
Matches 21; Conservative
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APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
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100.0%; Pred. No. 1.2e-09;
htive 0; Mismatches 0;
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FILE REFERENCE: 481112.404C2
CURRENT APPLICATION NUMBER: US/08/914,479
CURRENT FILING DATE: 1997-08/409,270
PRIOR APPLICATION NUMBER: 08/409,270
PRIOR APPLICATION NUMBER: 07/945,860
PRIOR APPLICATION NUMBER: 07/945,860
PRIOR FILING DATE: 1992-09-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                             ; FEATURE:
; OTHER INFORMATION: LT-B-M24 hybrid molecule
US-08-914-479A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: LT-B-M24 hybrid molecule US-08-914-479-2
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GENERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
TITLE OF INVENTION: FOR GROUP A STREPTOCOCCAL VACCINE
FILE REFERENCE: 481112.404C2
FILE REFERENCE: 481112.404C2
Query Match
Best Local S
Matches 21
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GENERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
TITLE OF INVENTION: EOR GROUP A STREPTOCCCCAL VACCINE
FILE REFERENCE: 481112.404C2
CURRENT APPLICATION NUMBER: US/08/914,479A
CURRENT FILING DATE: 1997-08-19
CURRENT FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 2
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Best Local Similarity
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Best Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 08/409,270 PRIOR FILING DATE: 1995-03-23 PRIOR APPLICATION NUMBER: 07/945,860
                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1992-(NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                          LENGTH: 138
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                    Local Similarity hes 21; Conserv
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                 100.0%; Score 106; DB 13; ilarity 100.0%; Pred. No. 1.4e-09; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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US-09-756-983-18
; Sequence 18, Application US/09756983
; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
                                                                                                      . OTHER INFORMATION: Fusion constructs with US-09-756-983-18
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; OTHER INFORMATION: Fusion constructs with human and US-09-756-983-15
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US-09-756-983-15
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LENGTH: 313
TYPE: PRT
                 Query Match
Best Local Similarity
                                                                                                                                                                                                               SEQ ID NO 18
LENGTH: 351
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION, TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS FILE REFERENCE: 246/285-CIP US/09/756,983 CURRENT APPLICATION NUMBER: US/09/756,983 CURRENT FILING DATE: 2001-01-09 PRIOR APPLICATION NUMBER: 60/105,018 PRIOR APPLICATION NUMBER: 60/105,018 PRIOR FILING DATE: 1998-10-20 PRIOR APPLICATION NUMBER: 09/421,506 PRIOR APPLICATION NUMBER: 09/421,506 PRIOR APPLICATION NUMBER: 09/421,506 PRIOR APPLICATION NUMBER: PCT/US99/2466
                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/105,018
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: 09/421,506
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: PCT/US99/2466
PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 24
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                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-10-19
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CURRENT FILING DATE: 2001-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Albani, Salvatore
                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                   FEATURE:
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                    100.0%;
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100.0%; Pred. No. 4e-09;
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No. 4.6e-09;
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APPLICANT: Williams, Neil Andrew
APPLICANT: Williams, Neil Andrew
FITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine
FITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR PRILING DATE: 1999-09-07
SOFTWARE: MS DOS
SEQ ID NOS: 6
SOFTWARE: MS DOS
TYPE: PRT
ORGANISM: E. coli
FEATURE:
LOCATION: 45...65
OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivable f
OTHER INFORMATION: porcine E. coli
US-09-786-648-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09756983

GENERAL INFORMATION:

APPLICANT: Albani, Salvatore

ITILE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,

TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF

TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS

FILE REFERENCE: 246,2285-CIP

CURRENT APPLICATION NUMBER: US/09/756,983

CURRENT FILING DATE: 2001-01-09

PRIOR APPLICATION NUMBER: 609/105,018

PRIOR APPLICATION NUMBER: 09/421,506

PRIOR FILING DATE: 1998-10-20

PRIOR APPLICATION NUMBER: 09/421,506

PRIOR FILING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: POT/US99/2466

PRIOR FILING DATE: 1999-10-19

NUMBER OF SEO ID NOS: 24

SEOTMAKE: FASTSEQ for Windows Version 4.0

SEO ID NO 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Fusion constructs with human and bacterial sequences US-09-756-983-22
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US-09-756-983-22
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US-09-786-648-5
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Query Match 95.3
Best Local Similarity 95.3
Matches 20; Conservative
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Best Local Similarity 100.0%;
Matches 21; Conservative 0
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ORGANISM: Artificial Sequence
FEATURE:
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                  95.3%;
95.2%;
Score 101; DB 21; Pred. No. 9.3e-10; 0; Mismatches 1
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Pred. No. 4.9e-09;
, Mismatches 0;
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Maximum Match 100%
Listing first 45 summaries
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657	417	369	211	192	549	496	2359	890	855	855	855	855	782	782	492	376	483	385
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US-60-360-039-5448	US-09-540-209B-9466	US-10-138-701-36	US-09-540-209B-9908	US-60-360-039-10029	US-09-540-209B-6846	US-10-155-881-37499	US-10-155-881-28520	US-60-360-039-3507	US-10-099-700A-2	US-10-104-271-2	US-09-654-600A-2	PCT-US02-09039-2	US-10-097-340-312	PCT-US02-07826-312	US-10-155-881-18930	US-60-360-039-21922	US-60-360-039-18750	US-09-540-209B-5629
Sequence 5448, Ap	Sequence 9466, Ap	Sequence 36, Appl	Sequence 9908, Ap	Sequence 10029, A	Sequence 6846, Ap	Sequence 37499, A	Sequence 28520, A	Sequence 3507, Ap	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 312, App	Sequence 312, App	Sequence 18930, A	Sequence 21922, A	Sequence 18750, A	Sequence 5629, Ap

ALIGNMENTS

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FILE REFERENCE: ACTBIO.004A

CUBRENT APPLICATION NUMBER: US/10/110,364

CURRENT FILING DATE: 2002-04-05

PRIOR APPLICATION NUMBER: PCT/US00/27607

PRIOR APPLICATION NUMBER: 60/158,561

PRIOR APPLICATION NUMBER: 60/158,561

PRIOR FILING DATE: 1999-10-08

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 103
           US-10-110-364-13
US-10-110-364-13
Sequence 13, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO. 004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 1
US-10-110-364-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
CURRENT APPLICATION NUMBER: US/10/110,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (1)...(103)
OTHER INFORMATION: CTB variant from NCBI gene bank GI: 1421511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                            th 100.0%; Similarity 100.0%; 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                      Score 106; DB 6;
Pred. No. 5.2e-11;
Mismatches 0;
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RESULT 4
US-10-110-364-17
Sequence 17, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Handley, Harold H.
APPLICANT: Handley, Harold H.
APPLICANT: Healt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILLING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR PHILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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: LOCATION: (1)...(103)
: OTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235
: OTHER INFORMATION: (Ogawa 41 R35D).
US-10-110-364-13
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                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: VARIANT; LOCATION: (1)...(105)
; OTHER INFORMATION: CTB variant from NCBI gene bank GI: 2781121 (Ogawa; OTHER INFORMATION: 41).
US-10-110-364-12
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LENGTH: 105
TYPE: PRT
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Best Local
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PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR EILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
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TYPE: PRT
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                                                                                                                                                                                                                                                                                        100.0%; Score 106; DB 6; 100.0%; Pred. No. 5.3e-11;
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Pred. No. 5.2e-11;
Mismatches 0;
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US-10-110-364-6
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; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1395122
US-10-110-364-17
Sequence 6, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 21
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NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 124
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 123
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                             66 GATFQVEVPGSQHIDSQKKAI 86
                                                                                                                                                                                                                                   1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 GATFQVEVPGSQHIDSQKKAI 86
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                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                 100.0%; Score 106; DB 6; 100.0%; Pred. No. 6.5e-11; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 123;
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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(124)
; OTHER INFORMATION: CTB variant from NCBI gene bank GI: 48890 (classic
; OTHER INFORMATION: 569B).
US-10-110-364-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
NAME/KEY: VARIANT;
LOCATION: (1)...(124)
OTHER INFORMATION: CTB variant from NCBI gene bank GI: 808900
US-10-110-364-6
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Best Local Similarity 100.
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                                                                                 Matches
                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US00/27607 PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                      LENGTH: 124
TYPE: PRT
ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 124
TYPE: PRT
ORGANISM: Vibrio cholera
66
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                   1 GATFQVEVPGSQHIDSQKKAI 21
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GATFQVEVPGSQHIDSQKKAI 86
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Ewalt, Karla L.
                                                                               Conservative
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Pred. No. 6.5e-11;
                                                                                                Score 106; DB 6; Pred. No. 6.5e-11;
                                                                                 Mismatches
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Gaps

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RESULT 8 US-10-110-364-19 ; Sequence 19, A

Application US/10110364

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66 GATFQVEVPGSQHIDSQKKAI 86

1 GATFQVEVPGSQHIDSQKKAI 21

0;

Gaps

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; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(124)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 408996.
US-10-110-364-21
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; NAME/KEY: VARIANT
; LOCATION: (1)...(124)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1648865
; OTHER INFORMATION: (LT87).
US-10-110-364-19
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US-10-110-364-21
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PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 21
LENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 21, Application US/10110364 GENERAL INFORMATION:
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SEQ ID NO 19
LENGTH: 124
TYPE: PRT
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APPLICANT: Handley,
APPLICANT: Haaparar
    Matches
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Best Local Similarity 100.0%;
Matches 21; Conservative 0
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                         TYPE: PRT
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                                                                                                                                                                                                                   ORGANISM: Escherichia
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  Conservative
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                    100.0%;
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Score 106; DB 6;
Pred. No. 6.5e-11;
); Mismatches 0;
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                                        Length 124;
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  Indels
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  0;
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  Gaps
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  0;
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RESULT 12
US-10-110-364-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-141-627-2
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                                                                                                                                                                                 Query Match
Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/141,627
CURRENT FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 138
Sequence 22, Application US/10110364 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10141627 GENERAL INFORMATION:
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Best Local :
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TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER TITLE OF INVENTION: FOR GROUP A STREPTOCOCCCAL VACCINE FILE REFERENCE: 481112.404C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 125
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Escherichia coli
                                                                                                         Match 100.0%;
Local Similarity 100.0%;
                                                                                                                                                                                 Local Similarity 100 les 21; Conservative
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                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                 0;
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Pred. No. 7.4e-11;
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Pred. No. 6.6e-11;
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                                                                                                                                                                                                                    Length 138;
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APPLICANT: Handley, Harold H.
APPLICANT: Handley, Harold H.
APPLICANT: Ewalt, Karla L.
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 1090-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                  ; NAME/KEY: VARIANT
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 223254.
US-10-110-364-20
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                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 22
                                                                                Matches
                                                                                                   Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/158,561
                                                                                                                                                                                                                                                                                        LENGTH: 123
TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                         FEATURE:
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                                                                              Local Similarity 95.; hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GETFQVEVPGSQHIDSQKKAI
                     1 GATFQVEVPGSQHIDSQKKAI 21
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95.2%;
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95.2%;
85
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                                                                                                   Score 101; DB 6;
Pred. No. 4.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 6; Pred. No. 3.9e-10;
                                                                                Mismatches
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                                                                                                                     Length 123;
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                                                                                Gaps
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0;

RESULT

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APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
FITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT EPLICATION NUMBER: US/10/110,364
CURRENT EPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 16
LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1169505.
US-10-110-364-16
В
                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                     ; NAME/KEY: VARIANT; LOCATION: (1)...(124)
; COTHER INFORMATION: LTB variant from NCBI gene bank GI: 145833.
US-10-110-364-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-10-110-364-18
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Best Local Similarity 95.2
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 16, Application US/10110364 GENERAL INFORMATION:
                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A CURRENT APPLICATION NUMBER: US/10/110,364 CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
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PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                       ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                                                                                                                                                                                                     ENGTH: 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 GETFQVEVPGSQHIDSQKKAI 86
                     1 GATFQVEVPGSQHIDSQKKAI 21
                                                                                  20;
                                                                                  Conservative
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95.2%;
                                                                                                  95.3%;
                                                                              Score 101; DB 6; Length 124; Pred. No. 4.8e-10; O; Mismatches 1; Indels

 Mismatches

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Pred. No. 4.8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 124;
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                                                                                Gaps
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Search completed: July 3, 2002, 09:04:12 Job time: 652 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:56:32; Search time 46.57 Seconds
(without alignments)
43.330 Million cell updates/sec

Title: US-09-786-648-4
Perfect score: 106
Sequence: 106
Sequence: BLOSUM62
Gapop 10.0 , Gapext 0.5
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Minimum Maximum

DB seq

length: 0 length: 2000000000 Total number of hits satisfying chosen parameters:

283138

283138 segs, 96089334 residues

Searched:

Database: PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	2	1	Result
41	41	41	41	41	41	41	41.5	41.5	42	42	42	42	42	42.5	43	43	43	43	44	44	44	44.5	44.5	46	46	48	100	101	Score
38.7	38.7	38.7	38.7	38.7	38.7			•		•	39.6	•			40.6	٠	40.6		41.5	41.5	41.5	42.0	42.0	43.4	43.4	5	94.3	95.3	Query Match
380	313	229	228	154	128	91	1090	500	864	787	427	299	216	376	935	439	399	365	1742	255	91	650	374	574	374	392	124	124	Length
N	N	Ŋ	N	1	<u>-</u>	N	N	N	N	N	N	ν	2	ш	N	N	N	2	2	N	N	N	N	N	N	N	1	1	DB
C34080	E88216	B27806	D34080	UQDOR7	UQDOR	F81109	S11823	JC4022	T49574	G81692	JC5694	JG0178	F83962	S17246	AE2469	T49189	T46898	н69231	S76110	A86457	C96580	AG0733	D81715	C86400	T19866	T04150	XVVCB	QLECB	ID
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polyubiquitin 5 (c	0	ubiquitin (clone l	18	\	ubiquitin / riboso	conserved hypothet	alpha-dextrin endo	4-aminobutyrate tr	probable carnitine	inner membrane pro	stress-activated p	chitinase (EC 3.2.	hypothetical prote	chorismate synthas	onent			£O.	hypothetical prote	probable peptide c	hypothetical prote	probable bacteriop	7		hetical p	RAD23 protein homo	cholera enterotoxi	heat-labile entero	Description

gibberellin 20-ox	T01/51	N	367	37.7	40	σ
hypothetical prot	T24938	N	ω 	37.7	40	4.
peptide	C89848	2	330	37.7	40	ω
prôt	C96827	2	260	37.7	40	2
hypothetica	T34767	N	242	37.7	40	Н
hypothetical prote	T32894	N	227	37.7	40	0
һурс	G69903	N	105	37.7	40	9
1S66	н95167	2	79	37.7	40	80
IS66	C95152	2	79	37.7	40	7
mutI	S47598	N	862	38.2	40.5	6
hypothetical	T20566	2	2911	38.7	41	ú
һур	T01770	2	550	38.7	41	4
poly	A34080	N	532	38.7	41	w
yaal	S66056	Н	386	38.7	41	2
poly	A27806	ν	381	38.7	41	31
poly	B34080	2	380	38.7	41	0

ALIGNMENTS

Microb. Pathog. 2, 381-390, 1987	A;Cross-references: GB:S60731; NID:g408994; PIDN:AAC60441.1; PID:g408996 R;Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K.;	A; Molecule type: DNA A; Residues: 1-17,'C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124 <r< td=""><td>A;Status: preliminary; translated from GB/EMBL/DDBJ</td><td>153542; MUID: 93252225</td><td>REMS MICROUIDI. Lett. 100, 137-101, 1393 A, Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic</td><td>R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.</td><td>A;Cross=references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376</td><td>A; Molecule type: DNA A; Residues: 1-22 <re2></re2></td><td>A;Status: preliminary; translated from GB/EMBL/DDBJ</td><td>A;Reterence number: 14128/; MUID:8/280041 A:Accession: 14128/</td><td>J. Biol. Chem. 262, 10189-10194, 1987 A; Title: A functional interaction between the signal peptide and the translation appa</td><td>R; Ibrahimi, I.; Gentz, R.</td><td>A; Experimental source: plasmid ENT-R PCG86</td><td>A; Residues: 1-5, 'F', 7-17,'C',19-24,'S',26-27,'E',29-33,'H',35-63,'K',65-66,'A',68-122</td><td>A; Molecule type: DNA</td><td>A; Accession: I41194 A.scratus noriminary</td><td>141194; MUID:85156481</td><td>A.Telle C. Immun. 40, 73 //, 1700</td><td>R;Leong, J.; Vinal, A.C.; Dallas, W.S. Infact Tumin 18 73-77 1985</td><td>A;Cross-references: EMBL:M15363; NID:g148335; PIDN:AAA24792.1; PID:g148336</td><td>A; Residues: 1-27, 'E', 29-63, 'K', 65-124 <yam></yam></td><td>A; Accession: B36946</td><td>411 CHECK TO THE CHARLES THE CONTRACT OF C</td><td>J. BACTERIOL. 169, 1332-1337, 1997.</td><td>R; Yamamoto, T.; Gojobori, T.; Yokota, T.</td><td>A; Residues: 1-124 CAPL></td><td>A; Accession: A01820</td><td>A01820; MUID:81074965</td><td>Nature 200, 499-301, 1900</td><td>R;Dallas, W.S.; Falkow, S.</td><td>C; Accession: AO1820; B26946; I41194; I41287; I67744; A61475</td><td>C:Species: Escherichia coli</td><td>heat-labile enterotoxin chain B precursor - Escherichia coli</td><td>OLECH OLECH</td><td></td></r<>	A;Status: preliminary; translated from GB/EMBL/DDBJ	153542; MUID: 93252225	REMS MICROUIDI. Lett. 100, 137-101, 1393 A, Title: Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic	R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.	A;Cross=references: GB:M17101; NID:g146375; PIDN:AAA23973.1; PID:g146376	A; Molecule type: DNA A; Residues: 1-22 <re2></re2>	A;Status: preliminary; translated from GB/EMBL/DDBJ	A;Reterence number: 14128/; MUID:8/280041 A:Accession: 14128/	J. Biol. Chem. 262, 10189-10194, 1987 A; Title: A functional interaction between the signal peptide and the translation appa	R; Ibrahimi, I.; Gentz, R.	A; Experimental source: plasmid ENT-R PCG86	A; Residues: 1-5, 'F', 7-17,'C',19-24,'S',26-27,'E',29-33,'H',35-63,'K',65-66,'A',68-122	A; Molecule type: DNA	A; Accession: I41194 A.scratus noriminary	141194; MUID:85156481	A.Telle C. Immun. 40, 73 //, 1700	R;Leong, J.; Vinal, A.C.; Dallas, W.S. Infact Tumin 18 73-77 1985	A;Cross-references: EMBL:M15363; NID:g148335; PIDN:AAA24792.1; PID:g148336	A; Residues: 1-27, 'E', 29-63, 'K', 65-124 <yam></yam>	A; Accession: B36946	411 CHECK TO THE CHARLES THE CONTRACT OF C	J. BACTERIOL. 169, 1332-1337, 1997.	R; Yamamoto, T.; Gojobori, T.; Yokota, T.	A; Residues: 1-124 CAPL>	A; Accession: A01820	A01820; MUID:81074965	Nature 200, 499-301, 1900	R;Dallas, W.S.; Falkow, S.	C; Accession: AO1820; B26946; I41194; I41287; I67744; A61475	C:Species: Escherichia coli	heat-labile enterotoxin chain B precursor - Escherichia coli	OLECH OLECH	

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A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin A;Reference number: A61475; MUID:89180953
A;Accession: A61475
A;Molecule type: protein
A;Residues: 22-24,'S',26-27,'E',29-63,'K',65-66,'A',68-95,'A',97-122,'E',124 <TSU>A;Experimental source: strain 240-3
C;Complex: the heat-labile enterotoxin molecule contains one A chain and five or si C;Function:
A;Description: the biological activity of the toxin is produced by the A chain, which contains enterotoxin beta chain
C;Reywords: enterotoxin
C;Reywords: enterotoxin
F;1-21/Domain: signal sequence #status predicted <STG>
F;22-124/Product: heat-labile enterotoxin chain B #status predicted <MAT>
F;30-107/Disulfide bonds: #status predicted
A;Molecule type: DNA
A;Residues: 1-20,'Q',22-31,'Q',33-38,'H',40-49,'G',51-67,'T',69-124
A:Experimental source: classical biotype strain 569B
                                                                                                                A;Cross references: GB:AE004224; GB:AE003852; NID:g9655952; A;Experimental source: serogroup 01; strain N16961; blotype R;Shi, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J. Chinese Biochem. J. 9, 395-399, 1993
A;Title: Nucleotide sequence analysis of the gene encoding the R;Reference number: JC1078
                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001 C;Accession: S14624; S39238; S39241; H82196; JC1078; S17666; PC1010; A05130; R;Dams, E.; de Wolf, M.; Dierick, W. submitted to the EMBL Data Library, March 1991 A;Description: Correction of the cholera toxin nucleotide sequence of the Vil A;Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: enterote
C;Species: Vibrio cholerae
C;Date: 24-Apr-1984 #sequer
C;Accession: S14624; S39238
                                                                                             A; Reference number: A; Accession: JC1078
                                                                                                                                                                                                                                                                 A; Residues:
                                                                                                                                                                                                                                                                                       A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                   A; Reference number: A82035; A; Accession: H82196
                                                                                                                                                                                                                                                                                                                                                              A; Title: DNA Sequence of both chromosomes A; Reference number: A82035; MUID: 20406833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X76390;
A;Accession: S39241
A;Molecule type: DNA
A;Residues: 1-124 <LEW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           submitted to the EMBL Data Library, November 1993 A; Description: Structure and arrangement of the {\rm C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: S14623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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A; Residues: 1-124 < LEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Lebens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:X58786; NID:g48420; A;Experimental source: strain 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-124 < DAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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Best Local
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                                                                                                                                                                                                                                                            type: DNA
1-124 <HEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S39238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NID: g433856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 101;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN:CAA41593.1;
                                                                                                                                                                                                                                                                                                                                                                                 the cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
.9e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:CAA53973.1;
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I.; Sellers,
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Best Local
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A; Molecule type: DNA
A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Cross references: GB:X00171; NID:948347; PIDN:CAA24996.1;
A; Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A; Title: Covalent structure of the beta chain of cholera ent A; Reference number: A01819; MUID:78005537
A; Residues: A01819
A; Molecule type: protein
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69-90,'N',92-124 <
A;Description: involved in binding of the toxin t C;Superfamily: cholera enterotoxin beta chain C;Keywords: enterotoxin; toxin F;1-21/Domain: signal sequence #status predicted F;22-124/Product: cholera enterotoxin chain B #stF;30-107/Disulfide bonds: #status experimental
                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 22-38, 'H',40-42,'N',44-67,'T',
A; Experimental source: biotype Inaba 569B
A; Note: Asn-65 was partially deaminated to
C; Comment: The authors translated the codd
C; Cenetics:
C; Genetics:
A; Gene: VC1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Resloues. 2. 2. R;Takao, T.; Watanabe, H.; Shimonisni, i. Eur. J. Biochem. 146, 503-508, 1985
A;Title: Facile identification of protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Determination of the primary structure of cholera toxin B subunit. A;Reference number: A38033; MUID:78005536
A;Accession: A38033
A;Molecule type: protein
A;Residues: 22-38; H',40-42; 'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>A;Residues: 27-38; H',40-42; 'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>A;Note: the difference at residue 70 may be due to deamidation during prepa R;Nakashima, Y.; Napiorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-38, 'H',40-67, 'T',69-124 <DA2>
A; Cross-references: EMBL:X58785; NID:948888;
A; Cross-references: EMBL:X58785; NID:948888;
C: R; Ma, Q.J.; Liu, C.X.; Xiong, L.S.; Yu, X.Q.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci
A; Title: B subunit of Cholera toxin produced
                                                                                                                                                                     C; Function:
                                                                                                                                                                                           ciate noncovalently
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C; Complex: the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: A21910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Nakashima, Y.; Napiorkowski, P.;
FEBS Lett. 68, 275-278, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; MoLecule type: protein
A; Residues: 22-38, 'H', 40-41 <MAQ>
R; Mokkalanos, J.J.; Swartz, D.J.; Pearson,
Nature 306, 551-557, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: PC1010
A; Accession: PC1010
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.watanabe, H.; Shimonishi, Y.
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GATFQVEVPGSQHIDSQKKAI

Score; Pred.
0; Mis

Similarity

94.3%; 95.2%;

Conservative

Mismatches

Indels

0,

Gaps

0,

100; No. 4

DB 1; .3e-09;

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hypothetical protein C40H5.3 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C:Accession: T19866 R:White, S.
    hypothetical protein T17H3.2 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Accession: C86400 C;Accession: C86400 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H
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C;Superfamily: unassigned ubiquitin-related
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A; Introns: 44/2; 95/1; 178/1;
C; Superfamily: Caenorhabditis
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Plant Mol. Biol. 34, 557-562, 1997
A;Title: Characterization and expression of a rice RAD23
A;Reference number: 208695; MUID:97369378
A;Accession: T04150
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision
C;Accession: T04150
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8; Conservative
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42.18;
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elegans hypothetical protein C40H5
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C.J.; Federspiel, N.A.; Kaul, S.; White, Conway, A.B.; Conway, A.R.; Creasy, T.H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                      Length 374;
                                                                                                                                                                                                                                                                                               Indels
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                         0
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                         Alonso
          probable bacteriophage protein STY2026 [imported] - Salmonella C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change C;Accession: AG0733
R;Parkhill, J; Dougan, G; James, K.D.; Thomson, N.R.; Pickard th, T; Connerton, P; Cronin, A.; Davis, P.; Davies, R.M.; Dow
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RESULT AG0733

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N

Matches

Local Similarity nes 12; Conserv

Conservative

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Mismatches

5

5.

Gaps

1;

g

321

ASFPDFLPGSQHKEKVWIDSTKLAL ATFQVEVPGSQH----IDSQKKAI 21

345

th, T.; Connerton, P.; Croni, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001

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Simmonds,

3

Skelton, J Salmonella

enterica

se

Stevens,

#text_change

09-Nov-2001

enterica

subsp.

enteri

Pickard, D.; V .M.; Dowd, L.;

Wain, J.; ; White, N

N.; Farr

drug

resistant

A;Status: preliminary

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RESULT
D81715
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A;Molecule type: DNA
A;Residues: 1-574 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sancho, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                               R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; I, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis 1
                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein TC0328 [imported] - Chlamydia muridarum (strain
C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ωy
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                                                                                                                                           A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719
                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-374 <TET>
                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                          A; Reference number: A81500; A; Accession: D81715
                                                                                                                                                                                                                                                                                                                                              C; Accession: D81715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
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Nature 408, 816-820, 2000
                                                                                                                        A; Experimental source: strain Nigg (MoPn)
    Query Match
Best Local
                                                                                                       Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
10; Conserv
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  42.0%;
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Pred.
Score 44.5;
Pred. No. 20;
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; Kolonay, J.;
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                    Length
                        374;
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.; McClarty,
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Salzbe
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A86457

Arabidopsis thaliana (ricess) probable peptide chain release factor F10C21.2 - Arabidopsis thaliana (ricess) (ricess) Arabidopsis thaliana (mouse-ear cress) (ricession Arabidopsis thaliana (mouse-ear cress) (ricession Arabidopsis thaliana (ricession 02-Mar-2001 #text_change 02-No-C; Accession: A86457

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Creas
                                                                                                       Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, I Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, R.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Wh Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, ansen, N.F.; Hughes, B.; Huizar, L.

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; wait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; S. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Reference number: A86141; MUID:21016719

A;Accession: C96580
  A; Molecule t
A; Residues:
                                             A; Status: preliminary
                                                                A; Reference number: A86141; A; Accession: A86457
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C;Genetics:
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A; Map position:
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A; Residues: 1-91 <STO>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKTFNLEVKGSEIIQQVKNMI
  type: DNA: 1-255 <ST
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                                                                                         MUID:21016719
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Pred.
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                                                                                                                                                                                                                                                                                       C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dev
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Maiti, R.; Ma
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sy, T.H.;
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                                                                                                                                                                                                                                                                                       Alonso,
war, K.;
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war, K.;
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Matches Query Match Best Local

Conservative

6,

Mismatches

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Indels

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Gaps

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40.6%;

Score Pred.

43; No.

DВ 3**4**;

2,

Length 365

ATFQVEVPGSQHIDSQKKA Similarity 7; Conser

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A; Experimental C; Genetics:
A; Gene: MTH985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
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C;Accession: 376110
C;Accession: 376110
C;Accession: 376110
C;Accession: 376110
C;Accession: 
                                                                                                                                   A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A;Reference number: A69000; MUID:98037514
A;Accession: H69231
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;Residues: 1-365 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Geneti
A;Start
                                                                                                                                                                                                                                                                                                                                                      R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sensory transduction histidine kinase - Methanobacterium thermoautotrophicum C;Species: Methanobacterium thermoautotrophicum C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
S76110
                                                                                                             A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: H69231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H69231
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A; Cross-references: EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-1742 <
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C;Genetics:
A;Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: nucleic acid sequence not shown; translation not shown
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Best Local Similarity 42...
Matches 8; Conservative
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les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
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                                                                            GB:AE000872; GB:AE000666;
ce: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL:D63999; GB:AB001339; ide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S74322; MUID:97061201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GB:AE005172; NID:g10645493; PIDN:AAG21605.1;
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42.1%;
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Pred. No.
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Pred. No.
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ed. No. 16;
Mismatches
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9;
                                                                                                     NID:g2622082;
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                                                                                                             PIDN: AAB85482.1;
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91 GKTYSMEGPGIQDCDEHNKGL 111

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A;Accession.
A;Coession.
A;Status: preliminary
A;Katus: preliminary
A;Molecule type: DNA
A;Residues: 1-439 <RIE>
A;Residues: 1-439 <RIE>
A;Cross references: EMBL.AL163818; GSPDB:GN00061; ATSP:MAA21.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    queuine tRNA-ribosyltransferase (EC 2.4.2.29) [validated] - Zymomonas mobil N;Alternate names: tRNA quanine transglycosylase C;Species: Zymomonas mobilis C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 18-Aug-2000 C;Accession: T46898; T46899
                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                     kinesin heavy chain-like protein - Arabidopsis thaliana
N;Alternate names: protein MAA21.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
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T49189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Pathway: queuosine biosynthesis; tRNA modification C; Superfamily: queuine tRNA-ribosyltransferase C; Keywords: glycosyltransferase; magnesium; metalloprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 5-399 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-399 < REU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Reuter, K.; Ricner, R.
J. Bacteriol. 177, 5284-5288, 1995
A;Title: Sequence analysis and overexpression of the A;Reference number: Z24129; MUID:95394847
A;Accession: T46898
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                        A; Map position:
A; Introns: 39/3
                                                                                                                                                                                                                                                                                                                          A; Reference number: Z25018
A; Accession: T49189
                                                                                                                                                                                                                                                                                                                                                                 submitted to the Protein
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                                                                                                                                                                                                                                                                                                                                                                                                       C; Accession: T49189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: (EC 2.4.2.29) [validated, MUID: 95394847]; catalyzes the exchange of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDB;
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                                                                             Best
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Best Local
                                                                                            Query Match
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                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATFQVEVPGSQHIDSQKKAI 21
M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; to the Protein Sequence Database, April 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIFLVKIPGGELVDANRSA
                                                                                                                                                        39/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
8; Conserv
                                                         Similarity 38.3
8; Conservative
                                                                                                                                                      74/1; 97/3; 138/3; 147/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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38.1%;
                                                                           40.6%;
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Pred. No. 37;
7; Mismatches
                                                       Score 43; DB Pred. No. 41; 3; Mismatches
                                                                                                                                                        193/3;
                                                                           DB
41;
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                                                                                            Length 439
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                                                                                                                                                      273/3; 304/2; 341/3; 401/3
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R.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabatz DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
AE2469
                                                                                                                                                                                                                                                                                                                     A; Reference number: AB1807; A; Accession: AE2469
                                                                                                                                                                               A; Gene: all5309
                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                   A; Experimental source:
                                                                                                                                                                                                                     A;Cross-references: GB:BA000019; |
A;Experimental source: strain PCC
                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-935 < KUR>
                                                                                                                                                                                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: AE2469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species:
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                                                                             Query Match
Best Local S
Matches 8
601 GVTFKVELLDTQDQDNQQSSV 621
                                   1 GATFQVEVPGSQHIDSQKKAI 21
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                                                                             Similarity
8; Conser
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                                                                             Conservative
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                                                                                              40.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and regulator all5309 [imported] -
                                                                             Score 43; DB
Pred. No. 91;
7; Mismatches
                                                                                                                                                                                                                                        PIDN:BAB77008.1; PID:g17134448; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                             is a synonym of Nostoc sp. 14-Dec-2001 #text_change 1
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R;Jones, D.G.L.; Reusser, U.; Braus, G.H. Mol. Microbiol. 5, 2143-2152, 1991
A;Title: Molecular cloning, characterization A;Reference number: S17246; MUID:92114793
A;Accession: S17246
                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X60190; NID:g3386; PIDN:CAA42745.1; R;VOLCKaert, G.; Voet, M.; Verhasselt, P.; Defoor, E. submitted to the Protein Sequence Database, May 1996 A;Reference number: S64153 , A;Accession: S64162
                                                                                                                                                                                               A;Gene: SGD:ARO2; MIPS:YGL148w
A;Cross_references: SGD:S0003116; MIPS:YGL148w
                                                                                                                                                                                                                                                               A;Cross-references: EMBL:272670; NID:g1322731; A;Experimental source: strain S288C
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A; Residues: 1-376 < JON>
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C;Accession: S17246; S64162
                                                                                                            C;Keywords: phosphorus-oxygen lyase; transmembrane F;347-363/Domain: transmembrane #status predicted <
                                                                                                                                                          C; Superfamily: chorismate synthase
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258 GSGFQGVSVPGSKHND

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GATFQ-VEVPGSQHID 15

Search completed: July 3, 2002, 08:56:33 Job time: 233 sec

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OM protein - protein search, using sw model
                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Run on: July 3, 2002, 09:04:42; Search time 21.51 Seconds (without alignments) 37.802 Million cell updates/sec

Title: Perfect score: Sequence: US-09-786-648-4 106

Scoring table: 1 GATFQVEVPGSQHIDSQKKAI 21

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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TO ANY CRYSTALLOGRAPHY (3.04 ANGSTROMS). X-RAY CRYSTALLOGRAPHY (3.04 ANGSTROMS). MEDLINE=99185101; PubMcd=10085117; Matkovic-Calogovic D., Loregian A., D'Acunto M.R., Battistutta R., Tossi A., Palu G., Zanotti G.;	DISCUSSION OF SEQUENCE. DISCUSSION OF SEQUENCE. MEDLINE-95349400; PubMed-7623669; Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.; Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R.; "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae."; Mol. Microbiol. 15:1165-1167(1995).	[4] [4] [5] [5] [6] [7] [6] [7] [7] [7] [7] [7] [7] [7] [7] [7] [7	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=ISOLATE H10407; MEDLINE=93252225; PubMed=8486242; INDUE T., Tsuji T., Koto M., Imamura S., Miyama A.; "Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain H 10407.";	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-ISOLATE H10407; STRAIN-ISOLATE H10407; STRAIN-ISOLATE H10407; STRAIN-ISOLATE H10407; Yamamoto T., Tamura T.A., Yokota T., Takano T.; Your Tamamoto T., Tamura T.A., Yokota T., Takano T.; "Overlapping genes in the heat-labile enterotoxin operon originating from Escherichia coli human strain."; Mol. Gen. Genet. 188:356-359(1982).	[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=ISOLATE H74-114; MEDIIIE=85156481; PubMcd=3884513; Leong J., Vinal A.C., Dallas W.S.; Leong J., Vinal A.C., Dallas W.S.; "Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin."; Infect. Immun. 48:73-77(1985).	ELTH OK LIFE. ESCHERICHIA COLI. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; ESCHERICHIA. NCBI TaxID-562;	PISELI; 01-JAN-1990 (Rel. 13, Created) 01-JAN-1990 (Rel. 13, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15-JUL-1999 (Rel. 38, Last annotation update) HEST-Labile enterotoxin B chain precursor (LT-B, human) (LTH-B).	I H H H

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21-JUL-1986 (Rel. 01, Created)
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coli heat-labile toxin.";
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prINTS; pr00772; ENTEROTOXINB.
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        "Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin."; Infect. Immun. 48:73-77(1985).
                                            MEDLINE-85156481; PubMed=3884513; Leong J., Vinal A.C., Dallas W.S.;
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3L; J01646; AAB02982.1; -.
3L; S60731; AAC60441.1; -.
3L; X83966; CAAS8800.1; -.
3; 1LTR; 23-MAR-99.
3; 1LTR; 123-MAR-99.
in: pF001376; Enterotoxin_B: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced throusen the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no re
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InterPro; IPR001835; Enterotoxin_B pfam; PF01376; Enterotoxin_B; 1. PR101772; ENTEROTOXINB.

ProDom;

PD012805;

Enterotoxin_B;

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=ISOLATE PCG86;
MEDLINE=87137303;
PubM
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PIR; A01820; Q
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[7]
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from E. coli.";
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P01556; Q9JQ02;
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13-AUG-1987 (Rel. 05, La
16-CCT-2001 (Rel. 40, La
Cholera enterotoxin, bet
CTXB OR TOXB OR VC1456.
                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-EL TOR 2125; Dams E., de Wolf M., Submitted (MAY-1991)
SEQUENCE FROM N.A. STRAIN-1854 / O139-BENGAL; Yamamoto K., Do V.G.R.F.,
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MEDLINE=94237453; PubMed=8181723;
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"Cholera toxin genes: nuc
vaccine development.";
Nature 306:551-557(1983).
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Submitted
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-!- FUNCTION: THE BETA CHAIN AGGREGATE
                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
STRAIN=OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE=97376625; PubMed=9232653;
METRITLE E.A., Sarfaty S., Jobling M.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x-ray Crystallography (2.2 angstroms).
MEDLINE=94272319; PubMed=8003954;
Merritt E.A., Sarfaty S., van den Akke
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Nature 406:477-483(2000).
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MEDLINE-20406833; PubMed=10952301;
Heidelberg J.F.; Eisen J.A., Nelson
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                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                         NCBI_TaxID=9606;
                                                           Homo sapiens
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3CHB;
1CHP;
1CHQ;
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A01819; XVVCB.
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20; Conser
                  A., Mittrucker
d (SEP-1997) to
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12-AUG-98.
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08-MAR-96.
23-DEC-96.
01-APR-97.
01-AUG-96.
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                                          s (Human).
Metazoa; Chordata; C
Metazoa; Primates; (
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13957 MW;
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factor 6 (IRF-6).
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                  ., Antonio L., Ozato K., Mak T.W.; EMBL/GenBank/DDBJ databases.
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                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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R MGD; MGI:1859211; Irf6.
R InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
PRINTS; PR002357; INFFNREGECT.
ProDom; PD002355; IRF; 1.
SMART; SM00348.
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                                                                                                                          the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Mus musculus (Mouse).
Mus musculus (Mouse).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Interferon regulatory factor 6 (IRF-6).
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Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
-i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                   Grossman A., Mittrucker H.W., Antonio L., Mak
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
-!- SUBCELLULAR LOCATION: Nuclear (Potential).
-!- SIMILARITY: BELONGS TO THE IRF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           P97431;
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transcription regulation; DNA-binding; Nuclear protein DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT. SEQUENCE 467 AA; 53129 MW; 7E28F5E0F5BA4053 CRC64;
                                                                                                                                                                                                                                                                                          STRAIN-BALB/C;
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TGT_ZYMMO
P28720; Q602
01-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-96256303; PubMed-8654300; MEDLINE-96256303; PubMed-8654300; Romier C., Reuter K., Suck D., Ficner R.; "Crystal structure of tRNA-guanine transglycosylase: RNA modification "Crystal structure";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Queuine tRNA-ribosyltransferase (EC 2.4.2.29)
transglycosylase) (Guanine insertion enzyme).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reuter K.K.H., Ficher R.;
"Sequence analysis and overexpression of the gene encoding tRNA-guanine transglycosylase: biochemical characterization of the enzyme.";
J. Bacteriol. 177:5284-5288(1995).
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STRAIN-ATCC 31821 / ZM4 / CP4;
MEDLINE-92406015; PubMed=1526462;
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- SUBUNIT: MONOMER.
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7; Conservative
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TRNA-RIBOSYLTRANSFERASE FAMILY.
                                                                                   ACTIVITY.
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RESULT 7
AROC_YEAST
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Best Local
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01-DEC-1992 (Rel. 24,
30-MAY-2000 (Rel. 39,
Chorismate synthase
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SEQUENCE
STRALM-S288C / FY1769;
MEDLINE-97197983; PubMed-9046099;
Voet M., Defoor E., Verhasselt P., Riles L., Robben J., Volckaert "The sequence of a nearly unclonable 22.8 kb segment on the left chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A, TIP1, MRF1 genes and six new open reading frames.";
Yeast 13:177-182(1997).
                                                                                                                                                                                                                                      Jones D.G.L., Reusser U., Braus G.H.;
"Molecular cloning, characterization and analysis of the regulation of the ARO2 gene, encoding chorismate synthase, of Saccharomyces cerevisiae.";
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INIT_MET
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pfam; PF01702; TGT; 1.
                                                                                                                                                                    SEQUENCE FROM N.A
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1ENU; 19-APR-00.
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1WKD;
1WKE;
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L33777; AAA27705.1; ALT_INIT
Z11910; -; NOT_ANNOTATED_CDS.
1PUD; 07-JUL-97.
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    Created)
    Last sequence update)
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    Last annotation update
    Carriage

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Pred. No. 14;
7; Mismatches
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3D-structure.
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14;
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                                                                                               Volckaert G.;
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RESULT 8
Matches
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Best Local
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99Y5Y6; Q9H350; Q9HCA3; Q9BS01; Q9HB36;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2001 (Rel. 40, Last annotation update)

16-OCT-2001 (Rel. 40, Last annotation update)

Suppressor of tumorigenicity 14 (EC 3.4.21.-) (Matriptase) (Membrane-
type serine protease 1) (MT-SP1) (Prostamin) (Serine protease TADG-15)

(Tumor associated differentially-expressed gene-15 protein).

ST14 OR PRSS14 OR SNC19 OR TADG15.
                                      "Reverse blochemistry: Use of macromolecular protease inhibitors dissect complex biological processes and identify a membrane-type serine protease in epithelial cancer and normal tissue."; Proc. Natl. Acad. Sci. U.S.A. 96:11054-11061(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase; As
SEQUENCE
        SEQUENCE
                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A., Craik C.

Takeuchi T., Shuman M.A., Craik C.

Takeuchi T., Shuman M.A., Craik C.

Takeuchi T., Shuman M.A., Craik C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000453; Chorismate_Synt.
Pfam; PF01264; Chorismate_Synt; 1.
ProDom; PP002941; Chorismate_Synt; 1.
PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_2; 1.
PROSITE; PS00788; CHORISMATE_SYNTHASE_3; 1.
Lyase; Aromatic amino acid biosynthesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i-cofactor: Reduced Flavin.
-!- PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITH THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATH-1: SUBUNIT: HOMOTETRAMER (BY SIMILARITY)).
                                                                                                                                                                                     protease
                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
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                                                                                                                                                                    J. Biol.
                                                                                                                                                                                                  Lin C.Y., Anders J., Johnson M., Sang Q.A. "Molecular cloning of cDNA for matriptase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE CHORISMATE SYNTHASE FAMILY.
                                                                                                                                                                                                                                SEQUENCE FROM N.A.
WEDLINE=99303581; PubMed=10373424;
                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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L; X99960; CAA68214.1;
L; Z72670; CAA96860.1;
L; S17246; S17246;
S10003116; ARO2.
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Chem. 274:18231-18236(1999).
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Primates;
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62.58;
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Pred. No. 17;
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between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrictuse by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                  This SWISS-PROT entry is copyright. between the Swiss Institute of Bio
                                                                                                                                                                                                                                                                                                                                          Lin C.Y., Anders J., Johnson M., Dickson R.B.; "Purification and characterization of a comple and a Kunitz-type serine protesse inhibitor fr J. Biol. Chem. 274:18237-18242(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99303582; PubMed=10373425;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of a novel transmembrane serine protease in human prostate.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamaguchi N., Mitsui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genomic
                                                                                                                                                                            OR LYS AS THE P1 SITE.
SUBCELLULAR LOCATION: Type II membrane protein
SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DON
SIMILARITY: CONTAINS 2 CUB DOMAINS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALS
                                                                                                                                                                                                                                                                               FUNCTION: DEGRADES EXTRACELLULAR MATRIX. PROPOSED TO PLAY A ROLE IN BREAST CANCER INVASION AND METASTASIS. EXHIBITS TRYPSIN-LIKE ACTIVITY AS DEFINED BY CLEAVAGE OF SYNTHETIC SUBSTRATES WITH ARG
                                                                                                                                                              TRYPSIN FAMILY.
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PRINTS; PRO0722; CHYMOTRYPSIN.
PRINTS; PRO0761; LDLRECEPTOR.
SMART; SM00042; CUB; 2.
SMART; SM00042; LDLa; 3.
SMART; SM00192; LDLa; 3.
SMART; SM00192; LDLa; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01209; LDLRA_1; 2.
PROSITE; PS50268; LDLRA_1; 2.
PROSITE; PS50240; TRYPSIN_DOM; 1
PROSITE; PS50134; TRYPSIN_HIS; 1
PROSITE; PS00135; TRYPSIN_SER; 1. EMBL; EMBL; HSSP; EMBL; EMBL; InterPro; IPR000859; CUB.
InterPro; IPR001314; Chymotrypsin.
InterPro; IPR002172; LDL_recept_A.
InterPro; IPR001254; Trypsin. Pfam; Pfam; MEROPS; S01.302; EMBL; ; PF00431; CUB; ; PF00057; ld1_r ; PF00089; tryps AF118224; AAD42765.2; -.
AF133086; AAF00109.1; -.
AB030036; BAB20376.1; -.
AF057145; AAG15395.1; -.
BC005826; AAH05826.1; -.
AF283256; AAG13949.1; -.
P00763; LDPO. trypsin; ldl_recept_a; Glycoprotein; Hydrolase; Serine procease;

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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-aminobutyrate aminotransferase, mitochondrial precursor (EC 2.6.1.19) (Gamma-amino-N-butyrate transaminase) (GABA transaminase) (GABA aminotransferase) (GABA-AT).
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"Screening and sequence determination obrain 4-aminobutyrate aminotransferase.
Gene 155:185-187(1995).
   "4-aminobutyrate aminotransferase (GABA-transaminase)
J. Inherit. Metab. Dis. 22:414-427(1999).
-!- CATALYTIC ACTIVITY: 4-aminobutanoate + 2-oxogluta
                                                Nyhan W.L., Gibson
                                                           MEDLINE=99336116; PubMed=10407778; Medina-Kauwe L.K., Tobin A.J., De
                                                                                           VARIANT LYS-220
                                                                                                                                                                                   MEDLINE=95154329; PubMed=7851425;
                                                                                                                                                                                                   TISSUE-Liver;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                               Tobin A.J., K.M.;
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LDL-RECEPTOR CLASS A

LDL-RECEPTOR CLASS A

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LDL-RECEPTOR CLASS A
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P07206;
01-APR-1988
01-APR-1990
01-MAR-2002
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Transferase; Aminotransferase; Pyridoxal phosphate;
Neurotransmitter degradation; Mitochondrion; Transi
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HSSP; P80147;
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DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY DISEASE: DISEASE: DEFECTION, HYPOTONIA, PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA, PHENOTYPE AND FEG
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COFACTOR: PYRIDOXAL PHOSPHATE.
SUBUNIT: MONOMER (PROBBLE).
SUBCELLULAR LOCATION: Mitochondrial matrix.
TISSUE SPECIFICITY: LIVER > PANCREAS > BRAIN >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYPERREFLEXIA, LETHPABNORMALITIES.
SIMILARITY: BELONGS
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J. Bacteriol. 171:3673-3679(1989).

-i- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic linkages in pullulan and in amylopectin and glycogen, and the alpha-and beta-limit dextrins of amylopectin and glycogen.
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Mol. Cell. Biol. [4]
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"Structure of two developmentally regulated
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antibody.";
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P08618;
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CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN.
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                                                                                                                 use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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Hypothetical 43.8)
                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein CONFLICT
                                                                                                                               P54278;
01-OCT-1996
01-OCT-1996
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
        SEQUENCE FROM N.A.
TISSUE=Endometrial tumor;
MEDLINE=94352394; PubMed=8072530;
                                                        Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-191 FROM N.A.
Bookstein C., Edwards C.W., Hulett F.M.;
Submitted (JUN-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
Bacteria; Firmicutes; Ba
Bacillus/Staphylococcus
NCBI_TaxID=1423;
Nicolaides
                                                                                                         PMS1 protein h
                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96051385; PubMed=7584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                              Homo sapiens (Human)
                                                                                                                                                                                PMS2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YAAN_BACSU
                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 QLMGSQHVDNKEK
                                                                                                                                                                                                                                                                  6 VEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                           IEIPGSEAVKAEKEQV
                                                                                                                                                                                                                                                                                                                                                                                                D26185; BAA05262.1; -. M96156; AAA22892.1; -. Z99104; CAB11802.1; -.
                                                                                                                                                                                                                                                                                          Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:1-14(1994).
N.C., Papadopoulos N.,
                                                                                                                                                                                                                                                                                                                                                     386 AA;
                                                                                                                   (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 40, Last annotation updat
n homolog 2 (DNA mismatch repair
                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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30, Last sequal
40, Last anno
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                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                     43830 MW;
                                                                                                                                                                                                                                                                                                     38.7%;
                                                                                                                                                                                                                                                                                                                                                             Complete proteome
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Last annotation update)
protein in XPAC-ABRB in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      group; Bacillus.
                                                                                                                                                                                                                                                                                        Score 41; DB
Pred. No. 31;
8; Mismatches
                                                                                                                                                                                                                                                                                          8
                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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D921F3A0F6845EEE CRC64;
Liu
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repair p
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В.,
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 Wei
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                                                                                                                    protein
Y.-F., Carter
                                                                                                                                                                                                                                                                                          3
                                                                                                                                                                                                                                                                                                                 Length 386;
                                                                                                                       PMS2)
 X.C.,
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AC OCC OCC OCC RT RAAC
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HS74_CAEEL
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Matches 9
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Lescoe M.K., Kane M., Earibino C., Lipford J., Lindblom A.,
Tannergaard P., Bollag R.J., Godwin A.R., Ward D.C.,
Nordenskjoeld M., Fishel R., Kolodner R.D., Liskey R.M.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLY INVOLVED IN THE REPAIR OF MISMATCHES IN DNA.
-!- SUBUNIT: HETERODIMER OF PMSZ AND MLI-
-!- DISEASE: ASSOCIATED WITH FAMILIAL HEREDITARY NONPOLYPOSIS COLON
CANCER (HNPCC) (LYNCH SYNDROME). HNPCC IS ONE OF THE MOST COMMON
GENETIC DISEASES IN THE WESTERN WORLD, AND ACCOUNTS FOR 15% OF ALL
    SEQUENCE FROM N.A.
MEDLINE-89306577; PubMed-2744444;
Heschl M.F.P., Baillie D.L.;
"Identification of a heat-shock pseudogene
                                                                                           Caenorhabditis elegans
Eukaryota; Metazoa; Nen
Rhabditidae; Peloderina
                                                                                                                                                                P2016-24_CAEEL STANDARD;
P2016-25
P2016-25
01-FEB-1991 (Rel. 17, Last seq
01-FEB-1991 (Rel. 17, Last seq
15-JUL-1998 (Rel. 36, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002099; DNA_mis_repair.
InterPro; IPR003594; HATPase_c.
Pfam; PF011119; DNA_mis_repair; 1.
Pfam; PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U13696; AAA63923.1; -.
EMBL; U14658; AAA5390.1; -.
HSSP; P23367; 1BKN.
SWISS-2DPAGE; P54278; HUMAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruben S.M., Rosen C.A., Haseltine W.H., Fleischmann R.D., Fraser C.M., Adams M.D., Venter J.C., Dunlop M.G., Hamilton S.R., Petersen G.M., de la Chapelle A., Vogelstein B., Kinzler K.W.; "Mutations of two PMS homologues in hereditary nonpolyposis colon
                                                                            NCBI_TaxID=6239;
                                                                                                                                                    Heat shock 70 kDa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                       HSP-4 OR HSP70D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA repair;
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 371:75-80(1994).
                                                                                                                                                                                                                                                                                                      528 GSQEHVDSQEKA 539
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European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                     470
862 AA;
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20
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                                                                                           Peloderinae;
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95797
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                                                                                                         Nematoda; Chromadorea;
                                                                                                                                                                                                                                                                                                                                                                         38.
75
                                                                                                                                                                   Last sequence update)
Last annotation updat
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                                                                                             Caenorhabditis.
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pred. No. 88;
2; Mismatches
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P -> S (IN REF. 2).
; B60A605222CBBCAC CRC64;
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                                                                                                          Rhabditida; Rhabditoidea;
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Matches 6
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                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             elegans.";
Genome 32:190-195(1989).
-i- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
-i- SUBCELLULAR LOCATION: EDDONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. STRONG,
                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                               PROSITE; PS01036; HSP70_3; PAKTIAL. ATP-binding; Heat shock; Endoplasmic
                                                                                                                                                                                                                                                                        InterPro; IPR000886; ER_target.
InterPro; IPR010123; HSP70.
Pfam; PF00012; HSP70; 1.
PROSITE; PS00014; ER_TARGET; 1.
                                                                                                                                                                                                                                                                                                                             EMBL; M28528; AAA28076.1; -. HSSP; P19120; 3HSC.
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                                                                 TFEIDVNGILHVSAEDK
                                                                                      TFQVEVPGSQHIDSQKK
                                                                                                                Similarity
6; Conserv
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PS00329;
PS01036;
                                                                                                                                                                                285
288 AA;
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             July
                                                                                                                                                                                                                                 ; ER_TARGET; 1.
; HSP70_1; PARTIAL.
; HSP70_2; PARTIAL.
; HSP70_3; PARTIAL.
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31267
             ω
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35.3%;
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Pred.
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                                                                                                                   Mismatches
                                                                                                                              N 0
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33;
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                                                                                                                                          Length 288
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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB DB
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46
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1: sp_archea:*
2: sp_bacteria
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sp_rodent:*
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Q9RP15
Q56635
Q93V32
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Q57193 vibrio chol
Q9rp15 vibrio chol
Q56635 vibrio chol
Q546635 vibrio phag
Q94m01 vibrio phag
Q94f64 vibrio chol
Q91jb0 arabidopsis
Q99987 homo sapien
Q91gm2 oryza sativ
Q40742 oryza sativ
Q40742 oryza sativ
Q9nkd5 drosophila
Q9uam9 caenorhabdi
Q9uam9 caenorhabdi
Q9sxc9 arabidopsis
Q9pky2 chlamydia m
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004636 arabidopsis	٠.	Q9v9u6 drosophila	Φ			Q94hm6 oryza sativ	Q9p606 neurospora			Q9pke3 chlamydia m	. Q965w6 caenorhabdi				Q9k9z2 bacillus ha		Q9f517 zymomonas m	O27066 methanother	-	Q43098 psophocarpu	022511 vitis vinif	Q55583 synechocyst	Q91vd0 mus musculu	Q9n136 ovis aries	Q9qz17 mus musculu	c875	Q9c815 arabidopsis	Q9syf4 arabidopsis

ALIGNMENTS

ΣX	DR	DR	DR	DR	DR	DR	DR	DR	RL	RA	RC	RP	RN	RL	RA	RC	RP	RN	RL	RΤ	RT	RA	RX	RC	RΡ	RN	o X	ဂ္ဂ	SO	GN	DE	ď	ΡŢ	ဌ	ð t	Q57193	RESULT
		PRINTS; PR00772; ENTEROTOXINB.	Pfam; PF01376; Enterotoxin_B; 1.	InterPro; IPR001835; Enterotoxin_B.	HSSP; P01556; 2CHB.	EMBL; A00931; CAA00098.1;			z	Xu L.;		SEQUENCE FROM N.A.	[3]	iochem. J	Shi C., Cao C., Zhang J., Ma Q.;	STRAIN=CLASSICAL BIOTYPE 569B;	SEQUENCE FROM N.A.	[2]	Biochim. Biophys. Acta 1090:139-141(1991).	3.";	"Nucleotide sequence analysis of the CT operon of the Vibrio cholerae	Dams E., De Wolf M., Dierick W.;	MEDLINE=91355224; PubMed=1883840;		SEQUENCE FROM N.A.	[1]		Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.	Vibrio cholerae.		IN B PROTEIN (CTB) PR	(TrEMBLrel. 17, Last	(TrEMBLrel. 01,	01-NOV-1996 (TrEMBLrel. 01, Created)	Q57193;	57103 DEEL THINKEY: DET. 124	P.7 1

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CHAIN
SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                       Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis cassette from Vibrio cholerae KNIH002 isol Misainmurhag Hoiji 35:205-210(1999).
EMBL: AF175708; AAD51360.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                              Q9RP15
Q9RP15;
        "Comparison of cholera toxin genes strains 854 (0139-bengal) and S7 (C Submitted (APR-1994) to the EMBL/GE EMBL; D30052; BAA06289.1; -. HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                 Bacteria; Proteobacteria; NCBI_TaxID=666;
                                                                                                 Vibrio cholerae
                                                                                                                 CHOLERA
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PRINTS; PR00772; ENTEROTOXINB.
ProDom; PD012805; Enterotoxin_B; 1.
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                                               Honda T.;
                                                              STRAIN=S7
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EROTOXIN B-SUBUNIT.
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CHOLERA TOXIN B PROTEIN (CTB).

D6BF83FFF7924EA3 CRC64;
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Pred. No. 2.6
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Pred. No. 2.
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                                                                                          subdivision; Vibrionaceae; Vibrio
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                               ctxAB) of non-O1 vibrio cholerae (O37) from two outbreaks.";
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01-DEC-2001
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                                      CTXB.
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PRINTS; PR00772; El ProDom; PD012805; Signal. SIGNAL 1
Vibrio phage CTX.
Viruses; ssDNA viruses;
NCBI_TaxID=141904;
[1]
                                                                                                                                                                                                                                                                                                         Vaccine 12:1083-1089(1994).
Vaccine 12:1083-1089(1994).
EMBL; AB011677; BAA25726.1;
SEQUENCE 124 AA; 14028 M
                                                                                                                                                                                                                                                                                                                                             "Escherichia coli heat-labile a trace amount of the holotoxi vaccine.";
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=1032 (ENTEROTOXIGENIC);
MEDLINE=95091056; PubMed=7998417;
Tamura S., Asanuma H., Tomita T., Ko
Hattori N., Watanabe K., Suzuki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
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No. 2.6e-10;
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T., Aizawa C.,
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Bhattacharyyaa T., Nandy R.K., Nair G.B.;

The entire core region of the ctx-phi (ctx-prophage) in environmental strain of V. cholerae.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF414369; AAL09682.1; -.

SEQUENCE 124 AA; 13884 MW; 8D4C251591B16891 CRC64;
                                                                                                                                                            O9LJBO:
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EMB|CAB77996.1.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop spermatophyta; Magnoliophyta; eudicotyjedons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00772; ENTEROTOXINB.
PRODOM; PD012805; Enterotoxin_B; 1.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Microbiol Immunol 39:87-94(1995).
HSSP; P01556; 1XTC.
InterPro; IPR001835; Enterotoxin_B: 1.
Pfam; PF01376; Enterotoxin_B: 1.
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    SEQUENCE FROM N.A
                                                                                                                                               NCBI_TaxID=3702;
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Sequence features of the regions
TAC and BAC clones.";
DNA Res. 7:217-221(2000);
EMBL; AP000606; BAB01195.1;
SEQUENCE 552 AA; 63036 MW; 7
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01-JAN-1998
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 2.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Serine/threonine-protein kinase; T)
SEQUENCE 508 AA; 58126 MW; 157FBF8F48511AF4
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Genomics 45:327-331(1997).
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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Mezu J., Oku A., Jones M.H., Shimane M.;
"Identification of two novel human putative
VRK1 and VR K2, with structural similarity t
                                                                                                                                         Q9LGM2
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                                                                                                                                                                                                                                                                                                                        Mismatches
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F4 CRC64;
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ESTS AU056822(S20908).
Oryza sativa (Rice).
Eukaryota; Viridiplantae;

Streptophyta; Embryophyta;

Last Last

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Pfam; PF00240; ubiquitin; 1.
SMART; SM00115; UBA; 2.
SMART; SM00213; UBQ; 1.
PR0SITE; PS50053; UBIQUITIN_2; 1
SEQUENCE 392 AA; 41754 MW; B
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Q40742;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Ma
Ehrhartoideae; Or
NCBI_TaxID=4530;
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OSRAD23.
Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Strep
Eukaryota; Magnoliophyta; I
^~~matophyta; Magnoliophyta; I
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submitted (JUN-2000) to the EM

EMBL; AP002521; BAA96762.1; --

EMBL; AP002539; BAB08201.1; --

HSSP: Q06319; 1BUC.
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Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                       "Characterization and expression of Plant Mol. Biol. 34:557-562(1997). EMBL; U63530; AAB65841.1; -. HSSP; P54725; IDVO.
                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97369378; PubMed=9225866; Schultz T.F., Quatrano R.S.;
                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-NIPPONBARE;
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"Oryza sativa nipponbare(GA3) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki T.,
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Ehrhartoideae;
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PF02771;
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                     Similarity
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acyl-CoA_dh; 1.
Acyl-CoA_dh_M; 1.
Acyl-CoA_dh_M; 1.
Acyl-CoA_dh_N; 1.
Acyl-CoA_Dh_2; UNKNOWN_1.
AA; 46132 MW; 8D34E3698A8E6367
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                     45.3%;
                                                                                                                                                                                                                              Ubiquitin
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01,
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(GA3) genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptophyta;
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Last annotation update)
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                     Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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Pred. No.
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2; Mismatches
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7.6;
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5.6;
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                                           10;
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  7;
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                                      Length 392;
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Best Local S
Matches 9
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                                                                                                                                               Q9P4E0;
Q9P4E0;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
O1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-CCT-2001 (TrEMBLrel. 19, Last annotation updat
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Y, CN BW SP;

Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.

Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi M.R., Moshrefi M.

Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

Zieran L.L., Rubin G.M.;

Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AE003408; AAR44847.1; -.

EMBL, AE003408; AAR44847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw Celniker S., Rubin G.M.;

"An exploration of the sequence of a 2.9-Mb region of the genome corosophila melanogaster: the Adh region.";

Genetics 153:179-219(1999).
                                                                     Ustilago maydis (Smut fungus).
Ustilaginomycetes; Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes;
Ustilaginomycetidae; Ustilaginales; Ustilaginaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0028907; BG:DS01514.3.
Hypothetical protein.
SEQUENCE 395 AA; 43561 MW; AE4F
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STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed-10471707;
                                                 Ustilaginomycetidae;
NCBI_TaxID=5270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
  SEQUENCE
                                                                                                                                                                                                                                                                                                                        Q9P4E0
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|:||:|| :| : |: |
10 GSTFQIEVDSAQKVADVKRII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 OVEVPGSQHIDSQKKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 56.
9; Conservative
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB Pred. No. 11; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2,
                                                                                                                                                                                                                                                                                                                           PRT;
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a; Brachycera;
                                                                                                                                                                                                                  update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 395;
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                                                                                  Ustilago.
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RESULT
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Matches 8
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Best Local
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Mol. Plant Microbe Interact. 13:781-786(2000).
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES EMBL; AF197562: AAF86841.1;
HSSP; P24941-1879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00069; pkinase; 1.

SMART; SM00220; S_TKC; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                               Glycosidase; Hydrolase; Signal. SIGNAL 1 27 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Str
Spermatophyta; Magnoliophyta;
eurosids I; Fabales; Fabaceae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     049876 PRELIMINARY; PRT; 293 AA.
049876;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CLASS III CHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                            EMBL; Y16415; CAA76203.1; HSSP; P23472; 2HVM.
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1998) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Kinase; SEQUENCE 1166 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Andrews D.L., Egan J.D., Mayorga M.E., The Ustilago maydis ubc4 and ubc5 gen
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Constitutive and stress-induced from Lupinus albus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rodrigues-Pousada C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. ULTRA;
Regalado A.P., Vidal S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3870;
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MEDLINE=20331594; PubMed=10875339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lupinus albus (White lupine)
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142
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                                       GATFQVEVPGSQHIDSQKKAI
GIDFDIEAGGAQHYDELARAL
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                                                                                                                                                                                                                                                                                       PF00192; chitinase_2; 1.
E; PS01095; CHITINASE_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                       Similarity
8; Conser
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IPRO00159; RA.
IPRO02290; Ser_thr_pkinase
                                                                                                                                                                                                                                                                                                                                    IPR001579; Chitinase_2.
                                                                                                                                                                                                     28
293 1
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                                                                                                                                                                                                293 P
31128 MW;
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                                                                                                            38
38
                                                                                                                                                                                                                                                                                                                                                                                                                           the EMBL/GenBank/DDBJ databases. TO CHITINASE CLASS II (FAMILY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptophyta; Embry, ta; eudicotyledons;
162
                                          21
                                                                                  Score 46; DB Pred. No. 12; 4; Mismatches
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Pred. No. 47;
4; Mismatches
                                                                                                                                                                                                POTENTIAL.
DB1B21728F657F2F
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. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genisteae; Lupinus.
                                                                                                                               Length 293;
                                                                                                                                                                                                     CRC64;
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RESULT
Q9SXC9
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Q9U3M9
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Best Local Similarity
Matches 8; Conserv
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01-MAY-2000
01-MAR-2001
C40H5.3 PROTI
               SEQUENCE FROM N.A.
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
                                                                                                                                                 Vysotskaia V.S., Schwartz J.R., Yu G., Torlumi M., Lenz C., Liu S. Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.; "Arabidopsis thaliana chromosome 1 BAC T17H3 sequence."; Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence up
01-DEC-2001 (TYEMBLrel. 19, Last annotation
T17H3.2 PROTEIN (AT1G27520/T17H3_2).
Satou M., Sel
Yamamura Y.,
                                                                                                                                                                                                                                                                STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL; 281482; CAB03954-2; -.
SEQUENCE 374 AA; 42198 MW;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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ADP-ribosylating t
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ALIGNMENTS

RESULT AAY87463

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AAY87463 standard;

peptide;

21 A

E. coli heat labile

enterotoxin B-derived peptide,

SEQ ID NO:5

03-JUL-2000

(first entry)

AAY87463;

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ adjuvant; immune disorder; diarrhoea. Williams NA, 07-SEP-1999; WO200014114-A1. Escherichia coli. Heat labile enterotoxin subunit B; EtxB;
beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; (UYBR-) UNIV BRISTOL. 16-MAR-2000 2000-256943/22. Hirst TR 98GB-0019484. 99WO-GB02970

Page 15;

62pp; English

The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit

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RESULT
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CC They may also be used as an inhibitor for toxin-induced with an composition comman and composition comman and composition comman and composition comman and composition comman and composition comman and composition comman and composition composition of a composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composition composit
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                                 New modified forms of pertussis holotoxin - developed using crystalline forms of pertussis holotoxin and its complexes with other molecules
                                                                                                                                                                                                                                                                                                24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1; Bordetella pertussis vaccines.
                                                                                                                       WPI; 1995-132623/18
                                                                                                                                                                                                                                                                                                                                                               23-AUG-1994;
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94US-0251121.
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PE;
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24-AUG-1993;
31-MAY-1994;
       holotoxin. The pertussis holotoxin modification process comprises:

(1) identification of at least one amino acid (aa) residue of the holotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein structure and function; (2) effecting mutagenesis (by removing or replacing a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying pertussis holotoxin, by studying its 3-dimensional crystalline structure. Modifying the holotoxin, alters its biological properties.
                                                                                                                                                                                                                                                                              Read RJ,
Hazes B,
                                                                                                                                     A method has been developed of producing a modified pertussis holotoxin, involving analysis of the 3-dimensional form of the crystalline holotoxin. The pertussis holotoxin modification process comprises:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (PT), E. coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to PT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella pertussis infection.
                                                                                                                                                                                              Example 3;
                                                                                                                                                                                                                       New method for producing modified
                                                                                                                                                                                                                                                  WPI; 1999-579908/49
                                                                                                                                                                                                                                                                                                                      (CONN-) CONNAUGHT LAB (UYAL-) UNIV ALBERTA.
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93US-0110947.
94US-0251121.
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Pred. No. 1.5e-10;
; Mismatches 0;
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RESULT
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forming a complex with the holotoxin and which molecule is an effector molecule which is an adenine nucleotide and which site contributes to toxicity, cell binding or enzymatic activity of PT. The functional interacting site(s) are identified by analysing the three dimensional structure of crystalline PT, determined by x-ray crystallogaphy. The identified interacting site(s) are modified to alter toxicity, cell binding or enzyme activity of the PT. The methods can be used to alter biological activity such as toxicity, enzymatic activity, mitogenicity, cell binding and adjuvanticity of the PT. The three-dimensional structu of PT have functional and/or structural resemblance to other bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  holotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (a which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis holotoxin. The present sequence represents an ADP-ribosylating toxin B-subunit peptide used in the exemplification of the present
                                                                                                                                                                                                                   The invention relates to methods of preparing a pertussis holotoxin (PT) having a modified biological activity. One method comprises identifying at least 1 site in a PT that interacts with a molecule that is capable of
                                                                                                                                                                                                                                                                                                                                               Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites or a molecule with crystalline toxin and modifying the identified site
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
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Pred. No. 1.
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site; mitogenicity; adjuvanticity;
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Best Local S
Matches 21
                                                                                                                                                                                                                           The present invention describes a crystalline form of isolated pertussis holotoxin, in which the molecules of pertussis toxin have a three dimensional structure represented in the specification, complexed with a polysaccharide molecule capable of forming a complexed with a polysaccharide molecule capable of forming a complex with the holotoxin. The crystalline form of the pertussis holotoxin can be used in a comparison with other proteins which have functional resemblance to pertussis holotoxin with the aim of modifying other proteins. Identifying the unknown sites of toxicity by comparison with the three dimensional structure of pertussis holotoxin provides a with the three dimensional structure of pertussis holotoxin provides a second control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control o
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Hazes B,
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24-AUG-1993;
31-MAY-1994;
                                                           technique for detoxification of toxins to produce useful immunogenic but non-toxic analogues. It can also be used as a primary standard to measure the quantity, purity or efficacy of less pure compositions containing pertussis toxin. AAY68340 to AAY68385 represent peptides used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crystalline form of proteins which have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-136703/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY68365
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94US-0251121.
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Hazes B,
                                                                                                                   The present invention provides a method for producing a pertussis toxin (also designated lymphocytosis-promoting factor, histamine-sensitising factor and islet activating protein) with a modified biological activity, involving analysing the crystal structure of the protein to identify active sites which can then be modified. This may lead to an alteration in the toxicity, cell binding or enzyme activity of the toxin. This can be used in the production of immunoprotective analogues of pertussis toxin. Pertussis toxin is the cause of whooping cough following infection
                                                                                                                                                                                                                                         Modifying pertussis holotoxin to comprising analyzing crystalline of toxicity, cell binding or enzy
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24-AUG-1993;
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                                                                                        Sequence
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getfqvevpgsqhidsqkkai
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94US-0251121.
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                                                                                                                                                                                                                                          oxin to produce detoxified PT analogs,
talline structure of toxin, to identify
or enzyme activity of PT and modifying
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Pred. No. 1.5e-10;
; Mismatches 0;
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histamine-sensitising factor;
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RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        immunogen; autoimmune
infection; parasitic;
antidiabetic; neuropro
                    E. coli LTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant AB5B subunit protein comprising a mutation that alters number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                     29-JUN-2001
                                                                                                                       AAB62377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E. coli LTB
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                                                                                                                                                                                                                                                                                     getfqvevpgsqhidsqkkai
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                                                                                                                                                                        Protein;
                       variant
                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
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                    (GI: 223254).
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pressive; antiarthritic; vaccine; heat labile toxi
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                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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l.7e-10;
es 0;
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RESULT
AAB62373
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XX AAB6
AC AAB6
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KW Inmou
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Best Local
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                                                                                 AB5B subunit protein; mutation; recombinant; cholera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; LTB infection; parasitic; immunosuppressive; antiarthitic; antirheumatic; antidiabetic; neuroprotective; vaccine; heat labile toxin B; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AB5B subunit protein; mutation; recombinant; cholera toxin B; CTB; immunogen; autoimmune disease; neuron demyelinating disease; rCTB; LTB infection; parasitic; immunosuppressive; antiarthritic; antirheumatic; antidiabetic; neuroprotective; vaccine; heat labile toxin B; variant.
                                                                                                                                                                                                                                                                        AAB62373 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-OCT-1999;
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                                                                                                                                                                                                     29-JUN-2001
                                                                                                                                                                                                                                       AAB62373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating
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                                                                                                                                                                                                                                                                                                                                                                         1 GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                                                                                                                                        getfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                     LTB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 AA;
                                                   coli
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                    protein
                                                                                                                                                                                                   (first
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                                                                                                                                                                    variant
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 22;
Pred. No. 2.1e-10;
; Mismatches 0;
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                                                  Query Match
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                                                                                                                                              effective target ligand binding affinity. A recombinant AB5B subunit protein such as cholera toxin B protein (CTB) can be specifically covalently linked at lysines or cysteines to an immunogen or vaccine. Recombinant mutant CTB (rCTB) can be used in the treatment of autoimmune diseases e.g. rheumatoid arthritis, encephalomyelitis (or other neuron demyelinating diseases) and diabetes. The rCTB or other B subunits of the invention can also be used to induce tolerance to infection, e.g. parasitic infection. The present sequence represents a variant of the E. coli heat labile toxin B (LTB) protein.
                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                     The invention relates to a recombinant AB5B subunit protein compristions one mutation, where the mutation alters the number of amino a residues available for chemical modification as compared to a wild
                                                                                                                                                                                                                                                                                                                                                                                                                                         Recombinant AB5B subunit protein comprising a mutation that alters number residues available for chemical modification, useful for covalently linking to an immunogen or vaccine which can be used for
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 70; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-OCT-1999;
                                                                                                                                                                                                                                                                                                         AB5B subunit protein, and where the recombinant protein retains
                                                                                                                                                                                                                                                                                                                                                                                                                           treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               нandley нн,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ACTI-) ACTIVE BIOTECH AB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-OCT-2000;
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                               h 100.0%;
Similarity 100.0%;
21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune diseases
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 21
                                   0;
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                                 Score 107; DB 22;
Pred. No. 2.1e-10;
Mismatches 0;
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                                                               Length
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RESULT 1
AAB62375
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Handley HH,
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                                                                                                                                                                                                       AAB62375;
                                                                                                       Escherichia
                                                                                                                        antidiabetic;
                                                                                                                                                                                                                        AAB62375 standard;
                (ACTI-) ACTIVE BIOTECH AB
                                  08-OCT-1999;
                                                   05-OCT-2000;
                                                                   19-APR-2001
                                                                                     WO200127144-A2
                                                                                                                                  infection;
                                                                                                                                                   AB5B subunit
                                                                                                                                                                                      29-JUN-2001
                                                                                                                                         ımmunogen;
                                                                                                                                                                                                                                                                  coli LTB
                                                                                                                                 parasitic;
                                                                                                                                         it protein;
autoimmune
                                                                                                       coli.
                                                                                                                                                                   protein variant
Haaparanta T,
                                                                                                                                                                                    (first entry)
                                                    2000WO-US27607
                                                                                                                        neuroprotective;
                                 99US-0158561
                                                                                                                                                                                                                        Protein; 124
                                                                                                                                 immunosuppressive;
                                                                                                                                         disease;
                                                                                                                                                 mutation;
                                                                                                                                                                                                                                                                      86
Ewalt
                                                                                                                                                                   (GI: 145833).
                                                                                                                           ; recombinant; cholera toxin B; CTB; neuron demyelinating disease; rCTB; LTB neuron demyelinathritic; antinheumatic; pressive; antiarthritic; antinheumatic;
                                                                                                                        vaccine; heat labile toxin B;
                                                                                                                        variant.
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WPI; 2001-281974/29

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                                                                                                                                                                               Recombinant AB5B subunit protein comprising a mutation that alters the number residues available for chemical modification, useful for % \left( 1\right) =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 1\right\} =\left\{ 
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        Disclosure; Page
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Matches 21
                                                                                                                                                                    The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                    Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding an exotoxin and a nucleic acid affinity domain
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                                                        was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired,
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N-PSDB; AAF75712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       osal cell binding affinity domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                          9;
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                                                                                                                                                                                                                                                                                                                    57pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 107; DB 22;
Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        motif; nucleic acid delivery;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LTBpL
ucosal cell, and administering a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                             for achieving
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Best Local :
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Best Local
                                                                                                        The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response when the for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition comprising the protein variant.
                                                                                                                                                                                                                                     Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding an exotoxin and a nucleic acid affinity domain -
                                                                                         Sequence
                                                                                                                                                                                                                    Example 1; Fig 10; 57pp; English.
                                                                                                                                                                                                                                                                           WPI; 2001-211103/21.
N-PSDB; AAF75713.
                                                                                                                                                                                                                                                                                                                                                           18-AUG-2000; 2000WO-US22715
                                                                                                                                                                                                                                                                                                                                                                                               WO200111960-A1
                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic
                                                                                                                                                                                                                                                                                                      Welter
                                                                                                                                                                                                                                                                                                                                         18-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                Exotoxin mucosal cell nucleic acid affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant exotoxin protein variant LTBpLh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB73242 standard; Protein; 142 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comprising
                                                                                                                                                                                                                                                                                                                       (AGRI-) AGRIVAX INC
                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2001
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                  1 GETFQVEVPGSQHIDSQKKAI 21
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         getfqvevpgsqhidsqkkai 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Similarity 21; Conser
                                             Similarity 100
21; Conservative
                                                                                         142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                         99US-0149294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                         binding
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                                             0;
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                                           Score 107; D
Pred. No. 2.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              motif; nucleic acid delivery;
heat-labile enterotoxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 107; DB 22;
Pred. No. 2.3e-10;
; Mismatches 0;
                                           DB 22;
2.5e-10;
s 0;
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                                                             142;
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                                                                                                                                                                                                                                               motif of
                                           Gaps
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RESULT 14
AAB73243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
Exotoxin mucosal cell binding motif; nucleic acid delivery; nucleic acid affinity domain; heat-labile enterotoxin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid to mucosal cells, for inducing an immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding an exotoxin and a nucleic acid affinity domain -
                                                                                                                                   14-MAY-2001
                                                                                                                                                                                       AAB73244;
                                                                                                                                                                                                                                           AAB73244 standard; Protein; 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-211103/21.
N-PSDB; AAF75714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB73243 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising the protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 11; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AGRI-) AGRIVAX INC
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                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                       66 getfqvevpgsqhidsqkkai
                                                                                                                                                                                                                                                                                                                                                                                                                           1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 AA;
                                                                          exotoxin protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US22715
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                                                                                                                                                                                                                                                                                                                                                                          86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 107; DB 22;
Pred. No. 2.8e-10;
; Mismatches 0;
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heat-labile enterotoxin.
                                                                               LTB-Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Search completed: July 3, 2002, 08:54:57 Job time: 287 sec
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                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                        The present invention relates to recombinant exotoxin protein variants, which comprise an exotoxin mucosal cell binding motif and a nucleic acid affinity domain. The present sequence is one such protein variant. In the present invention the heat-labile enterotoxin (LT) of Escherichia coli was used as an exotoxin. LT is a member of the ADP-ribosylating exotoxin (bARE) family. The protein variants are useful for selectively delivering nucleic acid encodes an antigen to which the immune response when the nucleic acid encodes an antigen to which the immune response is desired, for selectively delivering a gene to a mucosal cell, and for achieving expression of a protein in a subject, by administering a composition comprising the protein variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel exotoxin protein variant useful as protein carrier for facilitating gene delivery, comprises a mucosal cell binding motif of an exotoxin and a nucleic acid affinity domain
                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-211103/21.
N-PSDB; AAF75715.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 12; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AGRI-) AGRIVAX INC.
                                                                            163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0149294.
                                                                                                                                             100.0%; Score 107; DB 22; 100.0%; Pred. No. 3e-10; tive 0; Mismatches 0;
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Maximum
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Perfect score:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-467-976-26
US-08-952-337-5
US-08-952-337-5
US-08-952-337-5
US-08-952-337-2
US-09-013-047-2
US-09-191-852-21
US-09-374-852-21
US-08-952-337-1
US-08-952-337-2
US-08-952-337-2
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US-08-952-337-2
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Sequence 35, Appl	Sequence 35, Appl	Sequence 5, Appli	Sequence 12, Appl	12,	Sequence 4, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 133, App	Sequence 133, App	Sequence 2, Appli	Sequence 30, Appl	Sequence 23, Appl	Sequence 2, Appli

ALIGNMENTS

; TOPOLOGY: linear
DEDNESS
amino acid
: LENGTH: 93 amino acids
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116) 595-1163
; TELEPHONE: (416) 595-1155
; TELECOMMUNICATION INFORMATION:
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TRATION NUMBER: 24
: NAME: STEWART, Michael I.
ATION NU
PLICATION DATA:
G-199
: APPLICATION NUMBER: US 08/110,947
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APPLICATION NUMBER: US/08/292,968
CATION DATA:
; SOFTWARE: PatentIn Release #1.0, Version #1.25
SYSTEM: PC-DOS/MS-DOS
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TYPE: F1
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Toronto
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ADDRESSEE: Sim & MCBurney
CORRECTOR DENCES: 45
INVENTION: P
CANT: HAZES, Bart
ARMSTRONG, Glo
KLEIN, Mic
: LOOSMORE, Sheer
: OOMEN, Raymond F
: COCKLE, Stephen
STEIN, Pene
APPLICANT: READ, Randy J.
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· Sequence Of Application HS/0800068
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US-08-292-968-26

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US-08-467-974-26
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                     Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/110 047
ANDITCATION NUMBER: US 08/110 047
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PRIOR APPLICATION NUMBER: US 08/467,536
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ATTORNEY/AGENT INFORMATION:
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y Match 100.0%; Score 107; DB 2; Local Similarity 100.0%; Pred. No. 2.7e-11; hes 21; Conservative 0; Mismatches 0;
                                                                                                                     LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                        TOPOLOGY:
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KLEIN, Michel H.
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                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                 US 08/110,947
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                                 Length 93;
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; LENGTH: 93 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-467-536-26
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RESULT 4
US-08-467-976-26
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FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 31-MAY-1994
PRIOR APPLICATION NUMBER: US 08/
PRIOR APPLICATION NUMBER: US 08/
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                       NAME: STEWART, Michael I.
REGIEVEN NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/292,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
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APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                  35 GETFQVEVPGSQHIDSQKKAI 55
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ZIP: M5G 1R7
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STEIN, Penelope E.
STEIN Stephen A.
                                                                                                                                      Conservative
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ite 701, 330 University Avenue
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                                                                                                                                                      Score 107; DB 2;
Pred. No. 2.7e-11;
                                                                                                                                      Mismatches
                                                                                                                                                                    Length 93;
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US-09-082-514-26; Sequence 26, A
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                                                                                             Patent No.
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                                                                             GENERAL INFORMATION:
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                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/467,9/6 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/292,968 FILING DATE: 22-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Relaction DATA:
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APPLICATION NUMBER: US 01
FILING DATE: 31-MAY-1994
PRIOR APPLICATION DATA:
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NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0
FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
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READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
KLEIN, Michel H.
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OOMEN, Raymond P.
LOOSMORE, Sheena
KLEIN, Michel H.
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STEIN, Penelope E.
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                  6) 55
595-1163
NO: 26:
                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                              100.0%;
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                                                                                                                                                                                                                                                               Score 107; DB 3; Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                            Length 93;
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                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08829026A Patent No. 5837825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                  APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter Jejuni Flagellin-Escherichia Coli LT-B Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:

CORRESPONDENCE Sim & McBurney

Those, 330 University Avenue
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Janelle S. Graeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: ARMSTRONG, Glen APPLICANT: HAZES, Bart
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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5
     APPLICATION NUMBER: FILING DATE: 18-AUG
                                                                                                                                                  COUNTRY:
                                                                                                                                                                         STATE:
                                                                                                                                                                                     CITY: Beltsville
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/082,514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                     GETFQVEVPGSQHIDSQKKAI 55
                                                                                                                                    20705
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JMBER: US/08/829,026A
18-AUG-1997
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NO: 26:
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US-08-952-337-6
; Sequence 6, Application US/08952337
; Patent No. 6019973
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; ORGANISM: Vibrio cholerae
US-08-952-337-5
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APPLICANT: HOLDGEN, Jan
APPLICANT: LODENS, MICHAEL R.
APPLICANT: LODENS, MICHAEL R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/00758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT ETLING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER TILING DATE: 1996-05-02
                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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LENGTH: 102
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/007/58
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1996-05-05
EARLIER FILING DATE: 1995-05-05
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acid
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Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                   1 GETFQVEVPGSQHIDSQKKAI 21
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95.2%;
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Pred. No. 1.5e-10;
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1 GETFQVEVPGSQHIDSQKKAI 21

Matches

Conservative

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Indels

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Gaps

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Query Match Best Local Similarity

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; MOLECULE TYPE: US-08-472-171-2
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 102
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 95.2
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                                                                                                                                                                                        TELEX: 065-24567 Simbas INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,171
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
AND: CHARACTON:
                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Express:
TITLE OF INVENTION: Genetics
                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 416-595-1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                        NAME: Stewart, Michael I.
REFERENCE/DOCKET NUMBER: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Toronto
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M5G 1R7
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                                                                                                                        linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expression Of Gene Products From Genetically Manipulated Strains Of Bordetella
                   94.48;
95.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.4%;
                                                                                                                                                                                                                                                                            1038-507 MIS:vg
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Score 101; DB 2; L
Pred. No. 3.3e-10;
""cmatches 1;
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Pred. No. 3
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3e-10;
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                                 Length 103;
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RESULT 11
US-09-013-047-2
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                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application Patent No. 5942418
GENERAL INFORMATION:
                                                                                                                                                                                                        Sequence 2,
                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMOTE, Sheena M.
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K
APPLICANT: Zealey, Gavin R
APPLICANT: Klein, Michel H
                                             NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 24,973
REFERENCE/FOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: OCTIV: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                     TOPOLOGY: liner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: Canada
          ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/894,526 FILING DATE: 01-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                           , Application US/09013047 5998168
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Toronto
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) 595-1163
NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                       94.4%;
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                                                                                                                                                                                                                                                                                                                                                                                     Length 103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Applic
Patent No. 6140082
GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 20; Conserv
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TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                            COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Expression Of Gene Products From TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 23-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 416-595-1155
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APPLICATION NUMBER:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                     STREET: 330 Ur
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45
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REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                    CLASSIFICATION:
                                   FILING DATE:
                                                      APPLICATION NUMBER:
                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stewart, Michael
                                                                                                                                                                                                                                                      330 University Avenue, 6th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sheena M
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                                                     US/09/374,597
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pred. No. 3.3e-10;
0; Mismatches 1;
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Length 103;

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US-09-191-852-21
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Best Local Similarity
                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                               NAME: FOX, David L.
REGISTRACION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: PO
TELECOMMUNICATION INFORMATION:
TELECHONE: 713-651-5151
                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/1:
FILING DATE: 24-OCT-1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEPAX: 416-595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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TOPOLOGY:
                                                                                                     TELEFAX:
                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1301 | CITY: Houston
                                                                                                                                                                                                                                                                                                                                 FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45 GATFQVEVPGSQHIDSQKKAI 65
            FOPOLOGY:
                                             LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: FEBRU
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1301 McKinney, Suite 5100
                                                                                                   713-651-5246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
VENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
              linear
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FEBRUARY 23, 1995
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                                                                                                                                                                                                                                                                           PCT/US95/13376
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Pred. No. 3.3e-10;
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GENERAL INFORMATION:
APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
                                                                                                                                                                                  US-08-952-337-1
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                                                                                                                                                                                                   RESULT
                                                                                                                                                 ; Sequence 1, Application US/08952337
; Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: PCT-US95-13376-21
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Best Local Similarity
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NAME: Jones, John w.

REGISTRATION NUMBER: 31,380
REFERENCE/DOCKET NUMBER: 3617
TELECOMMUNICATION INFORMATION:
TOJ-850-9909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 713-850-090
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-CCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jones, John W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pravel, Hewitt, Kimball & Krieger STREET: 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                       1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                      GATFQVEVPGSQHIDSQKKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000
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6 US-08-120-97A-26

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5 US-08-251-305A-3

11 US-08-784-218-3

12 US-08-829-026-5
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Compugen Ltd.
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Sequence 5, Appli
Sequence 10, Appl
Sequence 26, Appl
Sequence 26, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 5, Appli
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-09-708-427-5824	-09-252-991A-	-09-252-691C-6923	9-252-691-69	-09-689-980	-09-391-631-3	S-09-689-980-E	-09-391-631-3	-09-451-320-3	US-09-563-997-4	S-09-769-970-2	S-09-758-445-	S-09-786-648-3	-08-732-371A	32-371-	S-09-402-100-	S-09-402-100-	-09-423-493-	09-051-315	08582-	US01	09-760-234-	-09-470-124-5	÷0S99-30747-5	-09-756-98	-09-756-983-1	-09-756-983-1	S-08-914-479A-	S-08-914-479-2	S-09-470-124-5	T-US99-30747-5	S-09-836-43	-09-836-433-2	-09-836-433-1	S-08-817-906-	US-08-782-832-1	-08-393-334-2	US-09-786-648-4
equence 5824	equence 29252	6923	equence 6923,	e 801,		e 802, /	3104,	388	4	2,	415	Ψ	, ,	1,	4, Appl	2, Appl	2	e 2, Appl	4, 7	3, AI	7, Appl	e 57,	i7, z	•	18,	15,	2	2, 1	e 55,); , ,	Ņ	20,	14,	e 21,	e 15	2, Appl	Sequence 4, Appli

ALIGNMENTS

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; FEATURE:
; LOCATION: 45...65
; OTHER INFORMATION: isolated or synthetic
; OTHER INFORMATION: porcine E. coli
US-09-786-648-5
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-786-648-5
Sequence 5, Application US/09786648
GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Tragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: MS DOS
SEQ ID NO 5
LENGTH: 21
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/GB99/02970 PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/786,648 CURRENT FILING DATE: 2001-03-07
                                                                                                                                                                                                                                          LENGTH: 21
TYPE: PRT
                                                                                                                                                                                                                    ORGANISM: E. coli
    100.0%;
       Score 107; DB 21; Pred. No. 1.4e-10;
                                                                                                                                              EtxB beta4-alpha2 loop fragment derivabl
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Matches

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Mismatches

Length Indels

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Gaps

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US-08-110-947A-26; Sequence 26, Application US/08110947A; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                       APPLICANT: STEIN, Penelope E
APPLICANT: COCKLE, Stephen A
APPLICANT: OOMEN, Raymond P
APPLICANT: KLEIN, Michel H
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: FALLOW, Charles W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shoemaker and Mattare, Ltd.
                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: COCKLE, Stephen F
APPLICANT: OOMEN, Raymond P
APPLICANT: KLEIN, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KEAD, KONGY J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite 1203 Crystal Plaza I, 2001 Jefferson
STREET: Davis Hwy.
CITY: Arlington
STATE: Virginia
                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                             35
                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (703) 415-08: TELEX: 89-9456 LUKPAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Virginia COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 24-AUG-1993
                                                                                                                                                                                                                                                                                                                                1 GETFQVEVPGSQHIDSQKKAI 21
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                                                                                                                                                                         READ, Randy J
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
Shoemaker and Mattare, Ltd. ite 1203 Crystal Plaza I, 2001 Jefferson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Charles W
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 5;
Pred. No. 9.3e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 93;
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TELEPHONE: (703) 415-0810
TELEPAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
        APPLICATION NUMBER: US/08/251,121
FILING DATE: 31-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATE: US 08/110,947
APPLICATION NUMBER: US 08/110,947
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                        TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                          STREET: Suite CITY: Toronto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/110,947A FILING DATE: 24-AUG-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: FALLOW, Charles REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                             RY: Canada
M5G 1R7
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                                                                                                                                                                                                                                                                                                                         INVENTION:
                                                                                                                                                                                                                         Ontario.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08251121
                                                                                                                                                                                                                                                         Suite 701,
                                                                                                                                                                                                                                                                                                                                                                   STEIN, Penelope E. COCKLE, Stephen A. COMEN, Raymond P. KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Davis Highway
                                                                                                                                                                                                                                                                                                                                        HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                       ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     READ, Randy J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss: single
linear
                                                                                                                                                                                                                                                                         Sim & McBurney
24-AUG-1993
                                                                                                                                                                                                                                                                                                                        MODIFICATION OF PERTUSSIS
                                                                                                                                                                                                                                                         330 University Avenue
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STEWART, Michael

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                                                                                                                                             US-08-150-305A-3
                                                                                                                                                                                         TELEFAX: 202-504 ... 3:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
FRUGTH: 371 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08150305A GENERAL INFORMATION:
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Best Local 9
                                                                Matches
                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Meinersmann, Richard
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: CAMPLIOBACT
TITLE OF INVENTION: FLAGELLIN-E
                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-504-5676
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Graeter, Janelle S.
REGISTRATION NUMBER: 35,024
REFERENCE/DOCKET NUMBER: 04
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$\,2008/150,305A
FILING DATE: 12-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                        TELEPHONE: 202-504-5060
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 GETFQVEVPGSQHIDSQKKAI 55
 49
                                                                                                                                                                          TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1:
CLASSIFICATION:
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                                                                               Local
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                            GETFQVEVPGSQHIDSQKKAI 21
GETFQVEVPGSQHIDSQKKAI 69
                                                            ch 100.0%; l Similarity 100.0%; 21; Conservative 0;
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21; Conserv
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Room 413, Building 005, BARC-W
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Pred. No. 9.3e-10;
                                                            Score 107; DB 5;
Pred. No. 5.5e-09;
; Mismatches 0;
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US-08-784-218-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/784,218
FILIUM DATE: 16-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08829026 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                         APPLICANT: Meinersmann, Richard J.
APPLICANT: Khoury, Christian A.
TITLE OF INVENTION: Campylobacter
TITLE OF INVENTION: Flagellin-Esch
                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Graeter, Janelle S
REGISTRATION NUMBER: 35,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                          COUNTRY:
                                                                                                                                                                                  CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 GETFQVEVPGSQHIDSQKKAI 69
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STREET: ROOM 411, Building 005, BARC-W
                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                   ADDRESSEE:
APPLICATION NUMBER:
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oom 411, Building 005, BARC-W
                                                                                                                                                                                                                                                                         Campylobacter Jejuni
Flagellin-Escherichia Coli LT-B Fusion Protein
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US/08/829,026
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                                    #1.25
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RESULT 9
US-08-393-334-2
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US-09-786-648-4
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-504-5676
TELEPAX: 301-504-5060
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
                                                                                                                                          Sequence 2, Application US/08393334 GENERAL INFORMATION:
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LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 7438
CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
APPLICANT: LOOSMORE, Sheena M.
APPLICANT: YaCOOD, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression (
TITLE OF INVENTION: Genetically
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Tinothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B
TITLE OF INVENTION: Adjuvants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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  Expression Of Gene Products From Genetically Manipulated Strains Of Bordetella 56
                                                                                                                                                                                                                                                                                                                                                                  94.4%; Score 101; DB 21; 95.2%; Pred. No. 1.4e-09;
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Best Local Similarity
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                                                                                                                                                     ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: MASON, Hugh S.
APPLICANT: Haq, Tariq A.
APPLICANT: Haq, Tariq A.
TITLE OF INVENTION: PRODUCTION OF AN ORALLY IMMUNOGENIC
TITLE OF INVENTION: BACTERIAL PROTEIN IN TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                APPLICATION NUMBER: US/08/782,832
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
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LENGTH: 103 amino acids
TYPE: amino acid
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TELEPHONE: 416-595-1155
TELEPAS: 416-595-1163
TELERA: 416-595-1163
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 77027-9095
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                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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Kettelberger, Denise M.
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95.28;
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Pred. No. 1.1e-08;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 713-850-0909

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REFERENCE/DOCKET NUMBER:

REGISTRATION NUMBER:

33,924

36170/3

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RESULT 11
US-08-817-906-21
US-08-817-906-21, Application US/08817906; SEQUENCE 21, Application US/08817906; GENERAL INFORMATION:
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                                                                           Query Match
Best Local :
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TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    TELEFAX: 713-651-5246 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements, APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                             FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24-OCT-1995
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MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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                                                                         Local
                                                                                                                                                                                                                                                                                 NAME: FOX, DAVID L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: 36
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USA
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                                                              Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                          Score 101; DB 12;
Pred. No. 1.1e-08;
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Pred. No. 1.1e-08;
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                                                                                          Length 103;
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Sequence 20, Application US/09836433

GENERAL INFORMATION:
APPLICANT: Yuki, Yoshikazu
APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
FIITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION UMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 116
TYPE: PRT
OPCANISM: SUITABLE CONSTITUTE
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Sequence 14, Application US/09836433

GENERAL INFORMATION:
APPLICANT: Vuki, Yoshikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
FILE REFERENCE: Not Assigned
CURRENT APPLICATION NUMBER: US/09/836,433

CURRENT FILING DATE: 2001-04-16

NUMBER OF SEQ ID NOS: 49

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; ORGANISM: synthetic construct US-09-836-433-22
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                         GENERAL INFORMÁTION:
APPLICANT: VUKL, YOShikaZU
APPLICANT: VUKL, YOShikaZU
APPLICANT: UGKA, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AU
FILE REFERENCE: NOT ASSIGNED
CURRENT APPLICATION NUMBER: US/09/836,433
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 49
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SEQ ID NO 14
LENGTH: 103
TYPE: PRT
ORGANISM: Vibrio cholerae
                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0 SEQ ID NO 22
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Best Local Similarity 95.3
Matches 20; Conservative
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                                                                                                     LENGTH: 11
TYPE: PRT
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95.2%;
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Pred. No. 1.3e-08;
0; Mismatches 1;
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Pred. No. 1.1e-08;
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Sequence 55, Application PC/TUS9930747

GENERAL INFORMATION:
APPLICANT: Boyce Thompson Institute for Plant Research at Cor
TITLE OF INVENTION: Orally Immunogenic Bacterial Enterotoxins Expressed In
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: 4868/8542
CURRENT APPLICATION UMBER: PCT/US99/30747
CURRENT FILING DATE: 1999-12-22
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 55
LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia coli
Search completed: July 3, 2002, 09:03:21 Job time: 621 sec
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Maximum Match 100%
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are greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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Sequence 22, Appl
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ALIGNMENTS

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RESULT 2
US-10-110-364-20
Sequence 20, Application US/10110364
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
, NAME/KEY: VARIANT
; LOCATION: (1)...(103)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 494265.
US-10-110-364-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 21; Conservative (
             APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTER
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
CURRENT APPLICATION NUMBER: US/10/110,364
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ORGANISM: Escherichia
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                                                                                                                                                                                                                                         GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                      Score 107; DB 6;
Pred. No. 6.3e-11;
                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                      Length 103;
                                                                                                                                                                                                                                                                                                                     Indels
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US-10-110-364-18

Sequence 18, Application US/10110364

GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITISE OF LINVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
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, NAME/KEY: VARIANT
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 223254.
US-10-110-364-20
                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                            US-10-110-364-16
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US-10-110-364-16
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                                                                                                                                                                                                                                                                                                      Best Local Similarity Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 16
LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application US/10110364 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
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APPLICANT: Ewalt, Karla L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/158,561
                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1169505
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                    100.0%; Score 107; DB 6; ilarity 100.0%; Pred. No. 7.9e-11; Conservative 0; Mismatches 0;
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Pred. No. 7.8e-11;
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; LOCATION: (1)...(124)
; OTHER INFORMATION: LTB
US-10-110-364-23
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                                                    Query Match
Best Local Similarity
Whiches 21; Conserva
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Best Local S
Matches 21
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APPLICANT: Handley, Harold H.
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 124
                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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                                                                                                                                                                                                                                                    ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                       TYPE: PRT
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ORGANISM: Escherichia
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                                                                                                                                                                                                                                                                                        LENGTH:
66
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                1 GETFQVEVPGSQHIDSQKKAI 21
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GETFQVEVPGSQHIDSQKKAI
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                                                                       Conservative
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                                                                                    100.0%;
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86
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                                                                                     Score 107; DB 6;
Pred. No. 7.9e-11;
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                                                                     Mismatches
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                                                                                                                                                                             bank GI:
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                                                                       Indels
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RESULT 6
US-10-110-364-10
IS-10-110-364-10
; Sequence 10, Application US/10110364
; GENERAL INFORMATION:
; APPLICANT: Handley, Harold H.

APPLICANT:

Haaparanta, Tapio Ewalt, Karla L.

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: NAME/KEY: VARIANT
: LOCATION: (1)...(103)
: OTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235
: OTHER INFORMATION: (Ogawa 41 R35D).
US-10-110-364-13
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COTHER INFORMATION: CTB variant from NCBI gene bank GI: 1421511
US-10-110-364-10
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
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Best Local S
                                                                      Matches
                                                                                         Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 31
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TYPE: PRT
ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                                LENGTH: 10
TYPE: PRT
                                                                                                                                                                                                                                                                             ORGANISM: Vibrio cholera
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nes 20; Conserv
45 GATFQVEVPGSQHIDSQKKAI 65
                     1 GETFQVEVPGSQHIDSQKKAI 21
                                                                        20;
                                                                                                                                                                                                                                                                                                                    103
                                                                                       Similarity
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                                                                      Conservative
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95.2%;
                                                                                         94.48;
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Pred. No. 6.7e-10;
                                                                                       Score 101; DB 6;
Pred. No. 6.7e-10;
                                                                        Mismatches
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                                                                                                       Length 103;
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RESULT

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LOCATION: (1)...(123)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1395122
US-10-110-364-17
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US-10-110-364-17
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                                                                Query Match
Best Local S
Matches 20
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Best Local Similarity 95.2
Matches 20; Conservative
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SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 123
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ORGANISM: Vibrio cholera
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(105)
OTHER INFORMATION: CTB val
OTHER INFORMATION: 41).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Handley, Harold H. APPLICANT: Haaparanta, Tapio APPLICANT: Ewalt, Karla L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-04-05
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PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GETFQVEVPGSQHIDSQKKAI 21
1 GETFQVEVPGSQHIDSQKKAI 21
                                                                  Similarity 95.2
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTB variant from NCBI gene bank GI: 2781121 (Ogawa
                                                                                    94.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                              Score 101; DB 6; Length 123; 
Pred. No. 8.3e-10; 
0; Mismatches 1; Indels
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66 GATFQVEVPGSQHIDSQKKAI 86

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                                                                                                                                                                                                ; NAME/KEY: VARIANT; LOCATION: (1)...(124)
; COTHER INFORMATION: CTB variant from NCBI gene bank GI: 808900
US-10-110-364-6
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; ORGANISM: Vibrio cholera
US-10-110-364-2
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                                                                                           Matches
                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO \, 6 \,
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/10110364 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hasparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION UMBER: PCT/US00/27607
PRIOR PILING DATE: 2001-0-05
PRIOR PILING DATE: 2002-01-0-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR PILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 31 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 31
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                                                                                                                                                                                                                                                                                 ORGANISM: Vibrio cholera FEATURE:
                                                                                                                                                                                                                                                                                                                          LENGTH: 124
TYPE: PRT
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366 GATFQVEVPGSQHIDSQKKAI 86
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                            1 GETFQVEVPGSQHIDSQKKAI 21
                                                                                                               Local Similarity
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Ewalt, Karla L.
                                                                                         Conservative
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                                                                                                        94.4%;
95.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.4%; Score 101; DB 6; Length 124; 95.2%; Pred. No. 8.3e-10;
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                                                                                                           Score 101; DB 6;
Pred. No. 8.3e-10;
                                                                                         Mismatches
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                                                                                                                              Length 124;
                                                                                         Indels
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APPLICANT: Handley, Harold H.

APPLICANT: Handley, Tapio
APPLICANT: Ewalt, Karia L.

TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
US-10-110-364-19
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                                                                                                                                                                                                       SEQ ID NO 19
LENGTH: 124
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APPLICANT: Handley, Harold H.
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Best Local :
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TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTEI
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR PPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
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APPLICANT:
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                   NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: (LTB variant from NCBI gene bank GI: 1648865
OTHER INFORMATION: (LTB7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT LOCATION: (1)...(124) COTHER INFORMATION: CTB variant from NCBI gene bank GI: 48890 (classic OTHER INFORMATION: 569B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 31
                                                                                                                             ORGANISM: Escherichia coli FEATURE:
                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Vibrio cholera
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0;

Query Match Best Local Similarity

94.4%;

Score 101; DB 6; Pred. No. 8.3e-10;

Length 124;

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TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 2001-10-08
NUMBER OF SEQ ID NOS: 31
SEQ ID NOS: 31
LENGTH: 124
LENGTH: 124
TYPE: PRT
                                                                                                                                                                   APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 15
; LENGTH: 125; TYPE: PRT; GRANISM: Escherichia coli; FEATURE: FEATURE: NAME/KEY: VARIANT; LOCATION: (1)...(125); OTHER INFORMATION: LTB variant from NCBI gene bank GI: 3062900. US-10-110-364-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 408996.
US-10-110-364-21
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US-10-110-364-15
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Best Local Similarity 95.2
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 15, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21, Application US/10110364 GENERAL INFORMATION:
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Query Match 94.4%; Score 101; DB 6; Length 125; Best Local Similarity 95.2%; Pred. No. 8.4e-10; Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps
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Search completed: July 3, 2002, 09:04:12 Job time: 652 sec

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chan score greater than or equal to the score of the resu and is derived by analysis of the total score distri
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1: pir1:*
2: pir2:*
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4: pir4:*
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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XVVCB
A86457
T04150
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S01433
T01770
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and containing	41 38.3 313	protein B0495.8 [i
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	ALIGNMENTS	
83138	RESULT 1 QLECB	
	QLECE QUECE C:Species: Escherichia coli C:Species: Escherichia coli C:Species: Escherichia coli C:Date: 29-Jun-1981 #sequence_revision 29-Jun-1981 #text_change C:Accession: A01820; B26946; I41194; I41287; I67644; A61475 R:Dallas, W.S.; Falkow, S.	a coli xt_change 18-Jun-1999 61475
	m - m	toxin and Escherichia coli heat
	A; Residues: 1-124 <dal> R; Yamamoto, T.; Gojobori, T.; Yokota, T.</dal>	
ult being printed,	A; Title: Evolutionary origin of pathogenic determinan: A; Reference number: A26946; MUID:87137303 A; Accession: B26946	determinants in enterotoxigenic Escherichi
	G	PIDN:AAA24792.1; PID:g148336
Description	R:Leong, J.; Vinal, A.C.; Dallas, W.S. Infect. Immun. 48, 73-77, 1985	
heat-labile entero	A; Title: Nucleotide sequence comparison between heat-labile A; Reference number: I41194; MUID: 85156481	abile toxin B-subunit cistrons
probable peptide c RAD23 protein homo	A;Accession: I41194 A;Status: preliminary	
hypothetical prote hypothetical prote	A; Molecule type: DNA A: Residues: 1-5,'F',7-17,'C',19-24,'S',26-27,'E',29-3:	,'H',35-63,'K',65-66,'A',68-122
kinesin heavy chai genome polyprotein	A;Cross-references: GB:M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831 A;Experimental source: plasmid ENT-R PCG86	064.1; PID:g145831
conserved hypothet hypothetical prote	R;Ibrahimi, I.; Gentz, R. J. Biol. Chem. 262, 10189–10194, 1987	
probable carnitine genome polyprotein	A; Title: A functional interaction between the signal ticulum.	eptide and the translation appa
probable receptor- ubiquitin / riboso	A;Reference number: I41287; MUID:87280041 A;Accession: I41287	
ubiquitin / riboso hypothetical prote	A;Status: preliminary; translated from GB/EMBL/DDBJ	
ב פ	A; Residues: 1-22 < RE2>	
ubiquitin (clone 1	A;Cross-references: GB:MI/101; NID:g146375; PIDN:AAAZ3973.1; R;Inoue, T.; Tsuji, T.; Koto, M.; Imamura, S.; Miyama, A.	9/3.1; PID:91463/6 A.
polyubiquitin 5 (c	A; Title: Amino acid sequence of heat-labile enterotoxin f A; Reference number: I53542; MUID: 93252225	enterotoxin from chicken enterotoxigenic
polyubiquitin 5 (c polyubiquitin 7 (c	A;Accession: I67644 A;Status: preliminary; translated from GB/EMBL/DDBJ	
tenascin precursor probable peptide c	A; Molecule type: DNA A; Residues: 1-17,'C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',	'K', 65-66,'A', 68-122,'E', 124 <r< td=""></r<>
peptide chain rele stress-activated p	A;Cross-references: GB:SbU/31; NID:g408994; PIDN:AACb0441 R;Tsuji, T; Lida, T; Honda, T; Miwatani, T; Nagahama,	441.1; PID:g408996 ma, M.; Sakurai, J.; Wada, K.;

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subunit of a heat-labile enterotoxin

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R;Shi, C.H.; Cao, C.; Zhang, J.S.; Ma, Q.J.
Chinese Biochem. J. 9, 395-399, 1993
A;Title: Nucleotide sequence analysis of the gene encoding +h~ ...
A;Accession: JC1078
A;Molecule +m~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 24-Apr-1984 #sequence_revision 01-Sep-2000 #text_change 02-Feb-2001 C;Accession: S14624; S39238; S39241; H82196; JC1078; S17666; PC1010; A05130; R;Dams, E.; de Wolf, M.; Dierick, W. submitted to the EMBL Data Library, March 1991 A;Description: Correction of the cholera toxin nucleotide sequence of the Vil A;Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Molecule type: protein
A:Residues: 22-24, 'S', 26-27, 'E', 29-63, 'K', 65-66, 'A', 68-95, 'A', 97-122, 'E', 124 <
A:Experimental source: strain 240-3
C:Complex: the heat-labile enterotoxin molecule contains one A chain and five C:Function:
A; Molecule type: DNA A; Residues: 1-20, 'Q', 22-31, 'Q', 33-38, 'H', 40-49, 'G', 51-67, 'T', 69-124 A; Experimental source: classical biotype strain 569B
                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, Il, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
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                                                                                                                                                                                                                                                                                                A;Title: DNA Sequence of both chromosomes of the cholera A;Reference number: A82035; MUID:20406833 A;Accession: H82196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA 'A; Residues: 1-124 <LEW>
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A; Residues: 1-124 < LEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, November 1993 A; Description: Structure and arrangement of the \mathrm{C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N; Alternate names: enteroto
C; Species: Vibrio cholerae
C; Date: 24-Apr-1984 #sequer
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A; Reference number:
A; Accession: A61475
                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X58786; NID:g48420; PIDN:CAA41593.1; A;Experimental source: strain 2125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-124 < DAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: enterotoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M.; Holmgren,
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Pred. No. 5.9e-10;
; Mismatches 0;
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    Vibrio cholerae

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R;Dams, E.; de Wolf,
Biochim. Biophys. Act
A;Title: Nucleotide s
A;Reference number: S
A;Accession: S17666
                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Molecule type: protein
A; Residues: 22-38, 'H', 40-67, 'T', 69, 'E', 71, 'QS', 74-75, 'VE', 78-86, 'Q', 88-99, 'Q', 101-103
R; Takao, T.; Watanabe, H.; Shimonishi, Y.
Eur. J. Biochem. 146, 503-508, 1985
A; Title: Facile identification of protein sequences by mass spectrometry.
A; Reference number: A21910; MUID:85126976
                                                                                                                                                                                                                                                                                               A:Molecule type: protein
A:Residues: 22-38,'H','40-42,'N','44-67,'T','69-90,'N','92-124
A:Experimental source: biotype Inaba 569B
A:Note: Asn-65 was partially deaminated to Asp
C:Comment: The authors translated the codon TCA for residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Cross-references: GB:X00171; NID:g48347; PID
R; Kurosky, A.; Markel, D.E.; Peterson, J.W.
J. Biol. Chem. 252, 7257-7264, 1977
A; Title: Covalent structure of the beta chain
A; Reference number: A01819; MUID:78005537
A; Accession: A01819
F; 22-124/Product: <br/>
F; 30-107/Disulfide
                                                                                                      A; Description: involved in binding C; Superfamily: cholera enterotoxin
                                                                                                                                                                                 C;Complex: the cholera enterotoxin molecule contains clate noncovalently with the subunit B, an aggregate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein
A; Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>A; Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>A; Note: the difference at residue 70 may be due to deamidation during pla; Nakashima, Y; Napiorkowski, P.; Schafer, D.E.; Konigsberg, W.H.
FEBS Lett. 68, 275-278, 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 22-38, 'H', 40-41 <MAQ>
R; Mekalanos, J.J.; Swartz, D.J.; Pearson,
Nature 306, 551-557, 1983
A; Reference number: A93320; MUID:84068199
A; Accession: A05130
                                             F;1-21/Domain: signal sequence #status
                                                                           C; Keywords: enterotoxin; toxin
                                                                                                                                                                                                            C; Complex: the cholera
                                                                                                                                                                                                                                 A; Map position:
                                                                                                                                                                                                                                                            A; Gene: VC1456
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A; Accession: A21910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: PC1010
A; Accession: PC1010
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A; Residues: 1-38, 'H', 40-67, 'T', 69-124 <DA2>
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                          cholera
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Acta 1090, 139-141, 1991
de sequence analysis of the
r: S17665; MUID:91355224
  bonds: #status
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                             enterotoxin
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                  is predicted of chain B #sta
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                                                                                                                                                                                                                                                                                                               Tyr.
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Similarity
19; Conser

Conservative

0;

90

5 8

Score 95; DB Pred. No. 5.2e 0; Mismatches

ль 1.2e-08; 2;

Indels

0,

Gaps

0,

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C.Accession: A86457
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; ansen, N.F.; Hughes, B.; Huizar, L. A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. Rizzo, M.; Rooney, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H. A; Reference and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
RESULT 5
C96580 hypothetical protein F15I1.6 [imported] - Arabidopsis thallana C:Species: Arabidopsis thaliana (mouse-ear cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Schultz, T.F.; Quatrano, R.S.
Plant Mol. Biol. 34, 557-562, 1997
Plant Mol. Biol. 34, 557-562, 1997
A;Title: Characterization and expression of a rice RAD23 gene.
A;Reference number: 208695; MUID:97369378
A;Accession: T04150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAD23 protein homolog - rice
C;Speckes: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04150
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A; Map position: 1
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:U63530; NID:g1488296; PIDN:AAB65841.1; PID:g1488297
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A; Residues: 1-255 <S7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable peptide chain release factor F10C21.2 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Nov-2001 C;Accession: A86457
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                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local
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Best Local
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                                                                                                                                                                                     1 GETFQVEVPGSQHIDSQKKAI
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                                                                                                                                            GSTFQIEVDSAQKVADVKRII 30
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                                                                                                                                                                                                                                   Similarity 42.9
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
9; Conser
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42.9%;
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                                                                                                                                                                                                                                   Score 47; DB
Pred. No. 10;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                  homology
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Dewar, K.;
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C;Gene
A;Map
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C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C;Accession: C86400
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
kinesin heavy chain-like protein - Arabidopsis thaliana
N;Alternate names: protein MAA21.110
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                             RESULT
T49189
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
""" Conserv
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A;Molecule type: DNA
A;Residues: 1-574 <STO>
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A; Residues: 1-91 <STO>
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C;Accession: C96580
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10; Conserv
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                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                             43.0%;
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Pred. No.
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3.2;
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                                                                                                                                                                                                                                                                                                                        0;
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RESULT
S78364
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A; Residues: 1-2733 <BRE>
A; Cross-references: EMBL:X51939; NID:g58974; PID:g1334829
C; Superfamily: infectious bronchitis virus RNA-directed RNA polymerase
C; Keywords: nucleotidyltransferase; RNA biosynthesis
 A; Note: the nucleotide sequence was C; Genetics:
                                  A; Molecule type: DNA
A; Residues: 1-263 <KOW>
A; Cross-references: EMBL: 267753;
                                                                                                 R;Kowallik, K.V.; Stoebe, B.; Schaffran, I.; Kroth-Pan Plant Mol. Biol. Rep. 13, 336-342, 1995
A;Title: The Chloroplast Genome of a chlorophyll a+c-A;Reference number: 578238
A;Accession: 578364
                                                                                                                                                                                   conserved hypothetical protein 263 - Odontella sinensis chloroplast C;Species: chloroplast Odontella sinensis C;Date: 17-reb-1998 #sequence_revision 26-Feb-1998 #text_change 20-C;Accession: S78364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome polyprotein - murine hepatitis virus (strain A59)
N;Alternate names: protein 1b
N;Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C;Species: murine hepatitis virus, MHV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Jun-2000
C;Accession: S15760; S08652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T49189
R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, April 2000
                                                                                  A; Status: preliminary; nucleic
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A;Accession: S15760
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A; Accession: T49189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: The primary structure and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Bredenbeek, P.J.; Pachuk, C.J.; Nucleic Acids Res. 18, 1825-1832,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            frameshifting mechanism
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Best Local S
Matches 9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                           N
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                                                                                                                                                                                                                                                                                                                             ETFQNNVPNYQHIGMKR 1214
                                                                                                                                                                                                                                                                                                                                                           ETFQVEVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKTYSMEGPGIQDCDEHNKGL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39/3; 74/1;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97/3; 138/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                            42.1%;
52.9%;
                                                                                   acid
                                 NID: g1185127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Noten, A.F.H.; Charite, J.; Luytjes, W.; Weiss, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            Score 45; I
                   submitted to
                                                                                   sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                     I.; Kroth-Pancic, P.; Freier, U.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193/3;
                                                                                     not shown;
                                                                                                                                                                                                                                                                                                                                                                                       1.7e+02;
6;
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f
                                 PIDN:CAA91737.1; PID:g1185254
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                   the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the second open reading frame of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     200/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9;
                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2733;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 439;
                   EMBL Data Library, November
                                                                                                                                    containing Alga, Odontella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                   translation not shown
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                                                                                                                                                                                                       20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304/2;
                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                      sinens
                    1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T49574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T19866
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A; Molecule type: DNA
A; Residues: 1-864 <SCH>
A; Cross-references: EMB
                                                                                                                                                                                                                                                  C; Accession: T49574
R; Schulte, U.; Aign, V.;
submitted to the Protein
                                                                                                                                                                                                                                                                                              probable carnitine acetyl transferase FacC [imported] - Neurospora crassa N;Alternate names: protein B208.220 C;Specles: Neurospora crassa C;Specles: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Map position: X
A;Introns: 44/2; 95/1; 178/1; 234/3; 348/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C40H5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein C40H5.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Genome: chloroplast
C; Superfamily: conserved
C; Keywords: chloroplast
                                                                             A; Introns: 138/1
                                                                                          A; Map position:
                                                                                                                                           A; Experimental source:
                                                                                                                                                                                                                     A; Reference number: 225022
A; Accession: T49574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-374 <WIL>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data A; Reference number: Z19189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: T19866
R;White, S.
                                                                                                       A; Gene: NCSP: B208.220
                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: T19866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary;
                                                                                                                         Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 42...
Matches 8; Conservative
                Query Match
Best Local
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        GETFQVEVPGSQHIDSQKK 19
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 Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
8; Conser
                                                                                                                                                                                                                                                    Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, he Protein Sequence Database, May 2000
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                         EMBL: AL355930; GSPDB: GN00116; NCSP: B208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: Z81482;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                           BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translated
                41.1%;
42.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.18;
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                                                                                                                                           clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C40H5
                                                                                                                                                                                                                                                                                                                                                                                                                           248
                                                                                                                                           B208;
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              Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from
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Pred.
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 Mismatches
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                                                                                                                                           strain OR74A
                                                                                                                                                                                                                                                                                                 02-Jun-2000 #text_change 02-Jun-2000
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            DB
73;
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30;
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21;
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                              Length 864;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 374;
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 Indels
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                                                                                                                                                         . 220
                                                                                                                                                                                                                                                                   В.;
                                                                                                                                                                                                                                                                    Holland, R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CESP:C40H5.3
 0,
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Gaps
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ETFQVEVPGSQHIDSQKKA

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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 199
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: infectious bronchitis virus RNA-directed RNA polymerase C;Keywords: glycoprotein; nucleotidyltransferase; RNA biosynthesis F;269,304,785,1184,1287,1524,1842,2196,2575,2630,2645,2665/Binding site: carbohydrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M55148; NID:g331851; PIDN:AAA46458.1; PID:g331853 R;Lee, H.J.; Shieh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Virology 180, 567-582, 1991 A;Title: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding A;Reference number: A38547; MUID:91111976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: B36815
R;Lee, H.J.; Shieh, C.K.; Gorbalenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, submitted to GenBank, February 1991
A;Description: The complete sequence (22 kilobases) of murine coronavirus gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
C84726
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C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 11-Jun-1999
C;Accession: B36815
                                           QY
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Best Local Similarity
"~+~hes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: neither nucleotide nor complete amino acid sequence is given C; Comment: This protein may be translated as a la-lb polyprotein by a ribosomal framesh
뮹
                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-641 <STO>
                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A84420; A; Accession: C84726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: genomic RNA
A; Residues: 1-2731 <LEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: A36815
A; Accession: B36815
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N; Alternate names: 1b protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome polyprotein 1b -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DЪ
                                                                                                                                                                                                                         A; Map position:
                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE002093; NID:g4887748; PIDN:AAD32284.1; GSPDB:GN00139
                                                                                                 Matches
                                                                                                                                                                                                                                                  Gene: At2g31880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1198
     359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         541 QTFWADAPGDAKIDALRKA
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     GEVFKAELPGSNGKIIAVKKVI
                                                GETFQVEVPGSQ-HIDSQKKAI
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                                                                                              l Similarity
11; Conserv
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                                                                                                                     40.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41.1%;
69.2%;
     380
                                                21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                 Pred. No. 64;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1;
Pred. No. 2.5e+02;
                                                                                                                                         Score 43.5;
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                                                                                                                64;
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A;Cross-references: GB:M23750; GB:J02858; NID:g167940; PIDN:AAA33264.1; PID:g167941 C;Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homolog C;Keywords: protein biosynthesis; protein degradation; ribosome F;1-76/Product: ubiquitin #status predicted <MATI>
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C;Superfamily: ubiquitin/ribosomal protein CEP52; ribosomal protein CEP52 homology; u C;Keywords: DNA binding; protein biosynthesis; protein degradation; ribosome; zinc fi F;1-76/Product: ubiquitin #status predicted <UBI>F;1-76/Domain: ubiquitin homology <UBH>F;77-128/Product: ribosomal protein CEP52 #status predicted <RIB>F;77-128/Domain: ribosomal protein CEP52 homology <CPH>F;77-128/Region: zinc finger CCCC motif F;121-128/Region: nuclear location signal
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R;Mueller-Taubenberger, A.; Westphal, M.; Jaeger, E.; Noegel, A.; Gerisch, G.
FEBS Lett. 229, 273-278, 1988
A;Title: Complete cDNA sequence of a Dictyostelium ubiquitin with a carboxy-terminal A;Reference number: S00357; MUID:88152253
A;Accession: S00357
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C:Date: 30-Jun-1991 #sequence_revision
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MEDLINE=93240541; PubMed=8478941;
Sixma T.K., van Zanten B.A.M., Dauter Z., Hol W.G.J
"Refined structure of Escherichia coli heat-labile
close relative of cholera toxin.";
J. Mol. Biol. 230:890-918(1993).
                                                                                                                                                             "A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic reticulum.";
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MEDLINE-85156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison between heat-labile toxin B-subunit cistrons from Escherichia coli of human and porcine origin.";
Infect. Immun. 48:73-77(1985).
                                                                                                                                                                                                                                                                                               STRAIN-ISOLATE PCG86;
MEDLINE-87137303; PubMed-3546273;
MEDLINE-87137303; PubMed-3546273;
Yamamoto T., Gojobori T., Yokota T.;
"Evolutionary origin of pathogenic determinants in enterotoxigenic "Evolutionary origin of pathogenic determinants in enterotoxigenic escherichia coli and Yibrio cholerae Ol.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Amino acid sequence homology between cholera toxin and Escherichia coli heat-labile toxin.";
Nature 288:499-501(1980).
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MEDLINE=81074965; PubN
Dallas W.S., Falkow S.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Heat-labile enterotoxin B chain precursor (LT
MEDLINE=91238966; PubMed=2034287;
                             J. Mol. Biol. [6]
                                                                                                                                                                                                                                       SEQUENCE OF 1-22 FROM N.A. MEDLINE=87280041; PubMed=3301830;
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Bacteria; Proteobacteria;
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              -RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
                                                                                                                                                  Biol.
                                                                                                                                                                                                                                                                                   Bacteriol. 169:1352-1357(1987)
                                                                                                                                                   Chem.
                                                                                                                                                262:10189-10194(1987).
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"Identification of errors among database sequence entries and
comparison of correct amino acid sequences for the heat-labile
enterotoxins of Escherichia coli and Vibrio cholerae.";
Mol. Microbiol. 15:1165-1167(1995).

-i- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED BY
THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.

-i- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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1LTA; 3
1LTB; 3;
1LTG; 1;
1LTI; 1;
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1LTS; 3;
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GETFQVEVPGSQHIDSQKKAI
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Pr01376; Enterotoxin_B, 1.
S; PR00772; ENTEROTOXINB.
m; PD012805; Enterotoxin_B; 1.
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; 31-JAN-94.

; 31-JAN-95.

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; 17-AUG-96.

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"Crystal structure of the B subunit of Escherienterotoxin carrying peptides with anti-herpes
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"Overlapping genes in the heat-labile enterotoxin operon originating
from Escherichia coli human strain.";
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European Bioinformatics Institute. The by non-profit institutions as long lifted and this statement is not removed. Ities requires a license agreement (See send an email to license@isb-sib.ch).
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InterPro; IPRO011835; Enterotoxin_B; 1.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
ProDom; PD012805; Enterotoxin_B; 1.
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STRAIN-EL TOR 2125;
MEDLINE-84068199; PubMed-6646234;
MEDLINE-84068199; Swartz D.J., Pear
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Vibrio cholerae.
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PDB; 1
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EMBL;
                                         Lebens M., Holmgren J.;
"Structure and arrangement of the cholerae 0139.";
                                                                                                                                                                                                                      Lockman H., Kaper J.B.;
"Nucleotide sequence analysis of the cholerae enterotoxin.";
J. Biol. Chem. 258:13722-13726(1983).
                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=84061784; PubMed=6315707,
                                   FEMS
                                                                 STRAIN=4260B / SEROTYPE 0139;
MEDLINE=94237453; PubMed=8181723;
                                                                                                 Dams E., de Wolf M.,
Submitted (MAY-1991)
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S60731;
X83966;
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MEDLINE-20406833; PubMed=10952301;

Metdelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwi
Dodson R.J., Haft D.H., H.Okey E.K., Peterson J.D., Umayam
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Ve
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MEDLINE-78005537; PubMed-903363;
MUDALINE-78005537; Peterson J.W.
Murosky A., Markel D.E., Peterson J.W.
"Covalent structure of the beta chain
"Covalent structure of the beta chain
J. Biol. Chem. 252:7257-7264(1977).
                                                                                                                                                                                                                Hirst T.R., Hol W.G.J.;
"Structural studies of receptor binding protein Sci. 6:1516-1528(1997).
-I. FUNCTION: THE BETA CHAIN AGGREGATE
                                                                                                                                                                                                                                                                                                                                                                                                           Maulik P.R., Reed K.A., Lung The 2.4 A crystal structure of
                                                                                                                                                                                                                                                                                                              STRAIN=OGAWA 41 / CLASSICAL BIOTYPE; MEDLINE=97376625; PubMed=9232653;
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Maulik P.R., Reed R.A., Shipley G.G.;
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MEDLINE=78005536; PubMed=903362;
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MEDLINE-90245573; PubMed-2159623;

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Weiss S.R., Spaan W.J.M.;
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01-APR-97.
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(Rel. 15, Last sequence update)
(Rel. 39, Last annotation update)
d RNA polymerase (EC 2.7.7.48) (ORF1B).
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EMBL; X51939; CAA..

PIR; S08652; S08652.

PIR; $15760; $15760.

Transferase; RNA-directed RNA

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-i- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CO
-i- EUNCTIONAL PROTEIN: IT CONTAINS THE ACTIV
FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA,
SUBGENOMIC MRNAS AND PROGENY VIRION RNA.

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate -
                                                                                                                                                                                                                                                                                                                                                                                                                       {RNA}(N).
-i- MISCELLANEOUS: THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B-POLYPROTEIN BY A RIBOSOWAL FRAMESHIFTING MECHANISM.
-i- SIMILARITY: TO THE AVIAN CORONAVIRUS IBV RNA POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        frame of the polymerase gene of the coronavirus MHV-A59; a highly conserved polymerase is expressed by an efficient ribosomal frameshifting mechanism.";
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ETFQNNVPNYQHIGMKR 1214
                             ETFQVEVPGSQHIDSQK 18
                                                                                                                                                                                                                                                                                                  non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                             Similarity 52.9
9; Conservative
                                                                               52
                                                                            .98;
                                                                                                                                                                                                                       RNA
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                                                                                                                                           MW;
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                                                             Score 45; DB Pred. No. 69; 2; Mismatches
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POLYMERASE.
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F3ACC8EF20D20C41
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                                                                                           Length 2733;
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01-FEB-1996
16-OCT-2001
          use by non-profit institutions as long as modified and this statement is not removed. Usentitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                   Plant Mol. Biol. Rep. 13:336-342(1995).
-!- SUBCELLULAR LOCATION: Integral membrane
-!- SIMILARITY: BELONGS TO THE TATC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; stramenopiles;
Biddulphiophycidae; Eupod:
NCBI_TaxID=2839;
                                                                                                                                                                                                                                                                                                                                                                                                      Odontella sinensis
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kowallik K.V., Stoebe B., "The chloroplast genome o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Kowallik K.V., Stc
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protein ycf43 (ORF263).
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TRANSMEM 103 123
TRANSMEM 130 150
TRANSMEM 153 173
TRANSMEM 181 201
TRANSMEM 213 233
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TRANSMEM 241 261
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                                                                                                                                                                                                                       Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTERNITS; PR00267; INTERNITS; PD002355; IRF; 1.
SMART; SM00348; IRF; 1.
PROSITE; PS00601; IRF; 1.
                                                                                                                            Transcription regulation; DNA-binding; Nuclear protein.
DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
SEQUENCE 467 AA; 53129 MW; 7E28F5E0F5BA4053 CRC64;
                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001346; IRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF027292; AAB84111.1; EMBL; AL022398; CAA18545.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
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Mammalia; Eutheria;
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15-JUL-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-1998) to the EMBL/GenBank/DDBJ (-!- SUBCELLULAR LOCATION: Nuclear (Potential). -!- SIMILARITY: BELONGS TO THE IRF FAMILY.
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InterPro; IPR002033; UPF0032.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
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PE; PS01218; TATC; 1
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8; Conser
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30080
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Primates;
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40.08;
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41.28;
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      Score 44;
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RESULT 8
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InterPro; IPR001346; IRF.
Pfam; PF00605; IRF; 1.
PRINTS; PR00267; INTERNREGECT.
PRODOM; PD002355; IRF; 1.
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01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                              RRPB_CVMJH
P29982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the Swiss Institute of Bioinformat
the European Bioinformatics Institute. The
use by non-profit institutions as long
modified and this statement is not removed.
entities requires a license agreement (See
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                  Ol-ARR-1993 (Rel. 25, Created)
16-OCT 2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
RNA-directed RNA polymerase (EC 2.7.7.48) (OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00601; IRE; 1.
Transcription regulation; DNA-binding; Nuclear protein DNA_BIND 9 111 TRYPTOPHAN PENTAD REPEAT.
SEQUENCE 467 AA; 53106 MW; 68CCAA90680FEDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grossman A., Mittrucker H.W., Antonio L., Mak Submitted (OCT-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
SEQUENCE FROM N.A
                                           NCBI_TaxID=11144;
                                                                   Viruses; ssRNA positive-strand viruses, Coronaviridae; Coronavirus.
                                                                                                                 Murine coronavirus MHV (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00348; IRF;
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Mammalia; Eutheria;
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01-MAR-2002 (Rel. 41, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
Interferon regulatory factor 6 (IRF-6)
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                                                                                                                                                                                                                                                                                                                                                                        273 QVKFPGPEHITNEKQKL 289
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                                                                                                                 JHM).
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Dictyostelium discoideum (Slime mold).
Dictyostelium discoideum (Slime mold).
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                                                                         Biochemistry
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Virology 180:567-582(1991).

-i- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CO.

-i- FUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVE FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA,

SUBGENOMIC MRNAS AND PROGENY VIRION RNA.

-i- CATALYTIC ACTIVITY: N nucleoside triphosphate =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89352609; I
Ohmachi T., Giorda
                                                                                                                                                                                                                                                                                                               MEDLINE-88152253; PubMed=2831095;
Mueller-Taubenberger A., Westphal M., Jaeger E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                       SEQUENCE
                                                                                                                                                                                                                                                          terminal tail and
                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=44689;
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MISCELLANEOUS: THIS PROTEIN MAY BE TRANSLATED AS A 1A-1B POLYPROTEIN BY A RIBOSOMAL FRAMESHIFTING MECHANISM.

SIMILARITY: TO THE AVIAN CORONAVIRUS IBV RNA POLYMERASE.
                                                                                                                                                                                                                   Lett.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETFQNNVPNYQHI 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                       FROM
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                                                                              28:5226-5231(1989)
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a R., Shaw D.R.,
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n A., Lai M.M.C.;
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CYS/HIS-RICH.
HELICASE.
ATP (BY SIMILARITY).
AMW; 99463066B1776970 CRC64;
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MW;
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                                                                                                                  regulated Dictyostelium
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Mol. Cell. Biol.
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MISCELLANEOUS: UBIQUITIN IS SYNTHESIZED AS A POLYUBIQUITIN
PRECURSOR WITH EXACT HEAD TO TAIL REPEATS. SOME UBIQUITIN GENES
CONTAIN A SINGLE COPY OF UBIQUITIN FUSED TO A RIBOSOMAL PROTEIN
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Pfam; PF00240; ubiquitin; 1.
PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1. EMBL; EMBL; PROSITE; PS00299; PROSITE; PS50053; HSSP; P02248; 1UBI. DictyDb; DD05001; u L; M19666; AAA33261.1; M19491; AAA333269.1; M19492; AAA33326.1; M23748; AAA33262.1; M23749; AAA33263.1; M23750; AAA33264.1; protein; 76 76 11 AA; CAA28408 Polyprotein 48 UBIQUITIN_1; UBIQUITIN_2; ubqA 8538 76 11 ¥. ALT_TERM.
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P10039; P13132; O73584; O73585;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Tenascin precursor (TN) (Hexabrachion) (Cytotactin) (Neuronectin) (GMEM) (JI) (Miotendinous antigen) (Glioma-associated-extracellular matrix antigen) (GP 150-225).
Gallus gallus (Chicken).
Gukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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"Tenascin: cDNA cloning an
"EMBO J. 7:2977-2982(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by recombinant tenascin fragments Cell 59:325-334(1989).
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Proc. Natl. Acad.
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MEDLINE-88176910; PubMed=2451243;
Jones F.S., Burgoon M.P., Hoffman S.,
Edelman G.M.;
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ALTERNATIVE PRODUCTS: 3 ISOFORMS; 230 KDA (SHOWN HERE), 200 K
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PRODUCED IN A TISSUE-AND TIME-SPECIFIC MANNER DURING DEVELOPM
INDUCTION: BY TGF-BETA.
SIMILARITY: CONTAINS 13 5 EGF-LIKE DOMAINS.
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THE BETA AND GAMMA CHAINS OF FIBRINOGEN.
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EUNCTION: SAM (SUBSTRATE-ADHESION MOLECULE) THAT APPEARS TO INHIBIT CELL MIGRATION. MAY PLAY A ROLE IN SUPPORTING THE GROWT OF EPITHELIAL TUMORS. IS A LIGAND FOR INTEGRINS ALPHA-8/BETA-1, ALPHA-V/BETA-3 AND ALPHA-V/BETA-6.

ALPHA-9/BETA-1, ALPHA-V/BETA-3 AND ALPHA-V/BETA-6.

SUBUNIT: HEXAMERIC. A HOMOTRIMER MAY BE FORMED IN THE TRIPLE COILED-COIL REGION AND MAY BE STABILIZED BY DISULFIDE RINGS AT BOTH ENDS. TWO OF SUCH HALF-HEXABRACHIONS MAY BE DISULFIDE LINK WITHIN THE CENTRAL GLOBULE.
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                              ,; M23121; AAA49086.1;
,; X08031; CAB40811.1;
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INE-90030407; PubMed-2478295;
ng J., Beck K., Chiquet-Bhrismann
contrary functions of tenascin: c
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        Pfam; PF00008; EGF; 13.
Pfam; PF00147; flbrinogen_C; 1
Pfam; PF00041; fn3; 11.
SMART; SM00018; EGF; 10.
SMART; SM0001; EGF_like; 1.
SMART; SM00016; FBG; 1.
SMART; SM00060; FN3; 10.
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Best Local
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99Y5Y6; 09H3S0; Q9HCA3; Q9BS01; Q9HB36;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Suppressor of tumorigenicity 14 (EC 3.4.21.*) (Matriptase) (Membrane-
type serine protease 1) (MT-Sp1) (Prostamin) (Serine protease TADG-15;
(Tumor associated differentially-expressed gene-15 protein).

ST14 OR PRSS14 OR SNC19 OR TADG15.
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Mammalia; Eutheria;
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EMBL; AF118224; AAD42765.2;
EMBL; AF13086; AAF00109.1;
EMBL; AF030036; BABA20756.1;
EMBL; AF057145; AAG15395.1;
EMBL; AF057145; AAG15395.1;
EMBL; AF05826; AAG13949.1;
HSSP; P00763; IDPO.
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TISUE-Prostate;
Yamaguchi N., Mitsui S.;
Yamaguchi n., Mitsui S.;
"Molecular cloning of a novel transmembrane serine protease
"Molecular cloning of a novel transmembrane serine protease
"Molecular cloning of a novel transmembrane serine protease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cao J., Fan W., Zheng S.; "Genomic analysis of a novel human serine protease SNC19."; submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
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J. Biol. Chem. 274:18231-18236(1999).
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SUBCELLULAR LOCATION: Type II membrane protein (Probable)
SIMILARITY: CONTAINS 4 LDL-RECEPTOR CLASS A DOMAINS.
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InterPro; IPR000859; CUB. InterPro; IPR001314; Chymotrypsin. InterPro; IPR001772; LDL_recept_A. InterPro; IPR001254; Trypsin.

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PF00431; PF00057;

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ARCC_YEAST STANDARD; PRT; 376 AA.

P28/77;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
30-MAY-2000 (Rel. 39, Last annotation update)
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SMART; SM00192; LDLa; 3.

SMART; SM00192; TYP_SPC; 1.

SMART; SM00020; TYP_SPC; 1.

PROSITE; PS01180; CUB; 2.

PROSITE; PS01209; LDLRA_1; 2.

PROSITE; PS50068; LDLRA_2; 4.

PROSITE; PS50040; TRYPSIN_DOM; 1

PROSITE; PS00134; TRYPSIN_HIS; 1

PROSITE; PS00134; TRYPSIN_HIS; 1

PROSITE; PS00135; TRYPSIN_SER; 1

Signal-anchor; Glycoprotein; Hyd:

Transmembrane; Repeat.
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STRAIN=S288C / FY1769;
MEDLINE=97197983; Pubn
                                                                                              of the ARO2 gene, cerevisiae.";
                                                                                                             "Molecular cloning, charact
                                                                                                               MEDLINE=92114793; PubMed=1837329;
Jones D.G.L., Reusser U., Braus G.H.;
"Molecular cloning, characterization a
of the ARO2 gene, encoding chorismate
                                                                                                                                                                                                                                                                         Eukaryota; Fungi;
Saccharomycetales;
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Eukaryota; Fungi; Ascomyc
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  PubMed=9046099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39.3%;
                                                                                                                                                                                                                                                                   (Baker's yeast).
cota: Saccharomycotina; Saccharomycetes;
aromycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CUB 1.

CUB 2.

LDL-RECEPTOR CLASS A 1.

LDL-RECEPTOR CLASS A 2.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 3.

LDL-RECEPTOR CLASS A 4.

SERINE PROTEASE.

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CHARGE RELAY SYSTEM (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB Pred. No. 61; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Þ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> GTR (IN REF. 2).
> S (IN REF. 4).
> V (IN REF. 3).
                                                                                                                 and analysis of the regulation e synthase, of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Serine
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)R (TYPE-II MEMBRANE PROTEIN)
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InterPro; IPR000433; Chorismate_synt.

Pfam; PF01264; Chorismate_synt; 1.

PfoDom; PD002941; Chorismate_synt; 1.

ProDom; PD002941; Chorismate_synt; 1.

PROSITE; PS00787; CHORISMATE_SYNTHASE_1; 1.

R PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.

R PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.

R PROSITE; PS00789; CHORISMATE_SYNTHASE_3; 1.

SEQUENCE 376 AA; 40838 MW; AF3AF65605B91E8E CRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; P:
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                        P80404;
01-NOV-1995 (
01-FEB-1996 (
30-MAY-2000 (
                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
4-aminobutyrate aminotransferase, mitochondrial precursor (EC 2.6.1.19) (Gamma-amino-N-butyrate transaminase) (GABA aminotransferase) (GABA-AT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and formodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: 5-0-(1-carboxyviny1)-3-phosphoshikimate chorismate + phosphate.
-!- COFACTOR: REDUCED FLAVIN.
-!- PATHWAY: SEVENTH STEP IN THE BIOSYNTHESIS OF CHORISMATE WITH THE BIOSYNTHESIS OF AROMATIC AMINO ACIDS (THE SHIKIMATE PATH -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- INDUCTION: BY AMINO ACID STARVATION.
                                                     Osei Y.D., Churchich J.E.;
"Screening and sequence determination obrain 4-aminobutyrate aminotransferase
Gene 155:185-187(1995).
                                                                                                             SEQUENCE FROM N.A.
TISSUE=Brain;
MEDLINE=95237607; PubMed=7721088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIP1, MRF1 genes and six Yeast 13:177-182(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sequence of a nearly unclonable 22.8 kb segment on the left chromosome VII from Saccharomyces cerevisiae reveals ARO2, RPL9A, TIP1, MRFI genes and six new open reading frames.";
MEDLINE=95154329; PubMed=7851425
             SEQUENCE OF 368-465 FROM TISSUE=Liver;
                                                                                                                                                                                                                                   ABAT OR GABAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                            258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; X60190; CAA42745.1; -.; X99960; CAA68214.1; -.; Z72670; CAA96860.1; -. S17246; S17246.
                                                                                                                                                                                                                                                                                                                                                                                                                           GSGFQGVSVPGSKHND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                      Chordata;
Primates;
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58;
                         N.A.,
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Pred. No. 31;
1; Mismatches
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                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 376;
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                                               RFH_ECOLI
                                                                   RESULT
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Best Local
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RFH_ECOLI
P28369; P77246;
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or send a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Inherit. Metab. Dis. 22:414-427(1999).
-!- CATALYTIC ACTIVITY: 4-aminobutanoate +
semialdehyde + L-glutamate.
-!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- SUBUNIT: MONOWER (PROBABLE).
-!- SUBCELLULAR LOCATION: Mitochondrial mat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99336116; PubMed=10407778; Medinla-Kauwe L.K., Tobin A.J., De Meirleir L., Jaeken Nyhan W.L., Gibson K.M.;
"4-aminobutyrate aminotransferase (GABA-transaminase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                de Biase D., Barra D., "Primary structure and aminotransferase.";
                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000954; Aminotran_3.
Pfam; PF00202; aminotran_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L32961; AAA74449.1; HSSP; P80147; 1GTX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase;
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                                                                                                                                                                          ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: MONOMER (PROBABLE).
SUBCELLULAR LOCATION: Mitochondrial
TISSUE SPECIFICITY: LIVER > PANCREAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: DEFECTS IN ABAT ARE A CAUSE OF GABA-AT DEFICIENCY WHOSE PHENOTYPE INCLUDES PSYCHOMOTOR RETARDATION, HYPOTONIA, HYPERREFLEXIA, LETHARGY, REFRACTORY SEIZURES, AND EEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABNORMALITIES.
SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMINOTRANSFERASES
                                                                                                                                  TYRLLVPGSRHI-SQAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137150;
                                                                                                                                                                          TFQVEVPGSQHIDSQKKA
                                                                                                                                                                                                                     l Similarity
10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               non-profit institutions as long as its content is in no way d and this statement is not removed. Usage by and for commercial s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation
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                                                                                                                                                                                                                                                                                                                               500
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113
132
191
191
204
216
268
320
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                                                                                                                                                                                                                                                                                                                               ΑA;
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    degradation; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227:476-480(1995).
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1113
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500
357
220
                                                                                                                                                                                                                                       38.8%;
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                                                                                                                                    ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIVER > PANCREAS
                                                                                                                                                                          20
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                                                                                                                                                                                                                                                                                                                                            R -> K (IN GABA-AT DEFIC:
REDUCTION IN ACTIVITY).
/FIId=VAR_008883.
D -> H (IN REF. 2).
V -> L (IN REF. 2).
E -> G (IN REF. 2).
K -> Q (IN REF. 2).
K -> Q (IN REF. 2).
G -> R (IN REF. 2).
G -> R (IN REF. 2).
C -> G (IN REF. 2).
C -> G (IN REF. 2).
C -> G (IN REF. 2).
                                                                                                                                                                                                                                       Score 41.5;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4-AMINOBUTYRATE AMINOTRANSFERASE PYRIDOXAL PHOSPHATE.
                          PRT;
                                                                                                                                                                                                                                                                                                                               -> G (IN REF. 2).
-> H (IN REF. 2).
41199085693F80AD
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                          141 AA
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S > BRAIN >
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                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFICIENCY; 25%
                                                                                                                                                                                                                                                              Length 500;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIDNEY >
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"Peptidase D gene (pepD) of Escherichia coli K-12: nucleotide sequence, transcript mapping, and comparison with other peptidase genes.";
J. Bacteriol. 179.4641-4657.....
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STRAIN-K12 / W3110;

Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itoh T.,

Yamamoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara

Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi K.;

"Systematic sequencing of the Escherichia coli genome: analysis of

"Systematic sequencing of the Escherichia coli genome: analysis of

4.0 - 6.0 min (189,987 - 281,416bp) region.;

Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                       the polypeptide chain release factor f model for release factor structure."; Nucleic Acids Res. 20:4423-4428(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Davis K., Federspiel
Lashkari D., Lew H.,
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AE000132; AAC73340.1; -.
D83536; BAA77905.1; -.
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Q1-NOV-1997 (Rel. 35, Created)
Q1-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical 37.0 kDa protein B0495.8 in chromosome II.
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST YDL087C AND S.POMBE SPCC16A11.13.
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DOMAIN 104 107 POLY-GLN
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SEQUENCE 141 AA; 16177 MW; 9D2EBD9AF7A04831 CRC64;
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5: sp_invertebia
6: sp_mammal:*
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Q9RP15
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09rpl5 vibrio chol
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093v32 escherichia
094m01 vibrio phag
09r646 vibrio chol
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091jb0 arabidopsis
09c875 arabidopsis
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Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X88785; CAA41591.1; -.
EMBL; U25679; AAC34728.1; -.
EMBL; 00931; CAA00098.1; -.
HSSP; P01556; 2CHB.
HSSP; P01556; 2CHB.
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Q57193;
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STRAIN-CLASSICAL BIOTYPE 569B;
Shi C., Cao C., Zhang J., Ma Q.;
Chin. Biochem. J. 9:395-399(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CLASSICAL STRAIN 569B;
MEDLINE=9135224; PubMed=1893840;
MEDLINE=9135224; PubMed=1893840;
Dams E. De Wolf M. Dierlick W.;
"Nucleotide sequence analysis of the CT operon classical strain 569B.";
Classical strain 569B.";
Discript Medical Strain 569B.";
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHOLERA TOXIN B PROTEIN (CTB) PRECURSOR (CTB).
                                                                               InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CLASSICAL BIOTYPE 569B;
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NCBI_TaxID=666;
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CHAIN
SEQUENCE
        "Comparison of cholera toxin genes (ctxAB) of strains 854 (O139-bengal) and S7 (O37) from tw Submitted (APR-1994) to the EMBL/GenBank/DDBJ EMBL; D30052; BAA06289.1; -.
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01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and nucleotide sequence analysis of the cassette from Vibrio cholerae KNIH002 isolated in Misainmurhag Holji 35:205-210(1999).
EMBL; AF175708; AAD51360.1; -.
HSSP; P01556; 2CHB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9RP15;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2001 (TrEMBLrel. 17, Last annotation
CHOLERA ENTEROTOXIN B-SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae.
Bacteria; Proteobacteria;
NCBI_TaxID=666;
                                                                                                                             STRAIN-S7
                                                                                                                                                                                            Vibrio cholerae.
Bacteria; Proteobacteria;
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Shin H.J., Park Y.C.,
                                                                                              Honda T.;
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D6BF83FFF7924EA3 CRC64;
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NCBI_TaxID=141904;
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EMBL; AB011677; BAA25726.1;
SEQUENCE 124 AA; 14028 M
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Signal.
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MEDLINE=95091056; PubMed=7998417;
Tamura S. Asanuma H. Tomita T., Ko
Hattori N., Watanabe K., Suzuki Y.,
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STRAIN-1032 (ENTEROTOXIGENIC);
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Bacteria; Proteobacteria;
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01-JUN-2001 (TrEMBLrel. 13, Last se
01-JUN-2001 (TrEMBLrel. 17, Last an
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
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Bhattacharyyaa T., Nandy R.K., Nair G.B.;
"The entire core region of the ctx-phi (ctx-prienvironmental strain of V cholerae.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ EMBL; AF414369; AAL09682.1;

EMBL: AF414369; AAL09682.1;
Nezu J., Oku A., Jones M.H., Shimane M.; "Identification of two novel human putative serine/threonine VRK1 and VR K2, with structural similarity to Vaccinia virus (N_{\rm e})^{-1}
                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
PRODOm; PD012805; Enterotoxin_B; 1.
SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E
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Bacteria; Proteobacteria;
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0139.";
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MEDLINE=98008921; PubMed=9344656;
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                                                                                                                                                                                                                                                                        Chordata;
Primates;
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      Arabidopsis thaliana
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Q9LJB0;
01-OCT-2000
                                                                                                                               Sequence features of the TAC and BAC clones.";
DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                             STRAIN=COLUMBIA;
Kaneko T., Kato T.,
Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                        STRAIN=COLUMBIA;
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QVEIPASMEIDEETKAI
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EMBL/GenBank/DDBJ databases
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Last sequence up
                                             Score 52; DB Pred. No. 2.9; 2; Mismatches
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RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA White O., Alonso J., Altafi H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Gill J.E., Goldsmith A.D., Hass B., Hansen N.F., Hughes B., Huizar L.,
RA Kim C.J., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
PAN Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
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RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Conway A.B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA Militscher J., Miranda M., Nuguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
"Sequence and analysis of chromosome 1 of the plant Arabidopsis
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Q9C875;
Q9C875;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation updat
""POTHETICAL 27.6 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AC051630; AA651209.1; -.

InterPro; IPR000352; Pep_rel_factor_I.

Pfam; PF00472; RF-1; 1.

SEQUENCE 255 AA; 27445 MW; B54F389
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Pred. No.
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                                                                                                                                                                          clone:P0433F09.";

Submitted (JUN-2000) to the EMBL/Ge
EMBL; AP002521; BAA996762.1; -
EMBL; AP002539; BAB08201.1; -
HSSP; Q06319; 1BUC
InterPro; IPR001552; Acyl-CoA_dh, 1.
Pfam; PF00441; Acyl-CoA_dh_M; 1.
Pfam; PF02771; Acyl-CoA_dh_M; 1.
Pfam; PF02771; Acyl-CoA_dh_M; 1.
Pfam; PF02771; Acyl-CoA_dh_M; 1.
PF6am; PF02771; Acyl-CoA_dh_M; 1.
                                                                                                                                                                                                                                                                                      STRAIN=CV. NIPPONBARE Sasaki T., Matsumoto "Oryza sativa nipponb
                                                                                                                                                                                                                                                                                                                                                       Sasaki T., Matsumoto T., Yamar
"Oryza sativa nipponbare(GA3)
clone:P0041E11.";
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Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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01-OCT-2000
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EMBL; AC027035; AAG51290.1; -.
Interpro; IPR000352; Pep_rel_factor_I.
Pfam; PF00472; RF-1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel.
ESTS AU056822(S20908).
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01-DEC-2001
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V. NIPPONBARE;
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257 AA; 27645 MW;
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yl-coa_dh_N; 1.
acyt_coa_bh_2; unknown_1
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Pred. No.
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Pred. No.
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genomic
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annotation
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InterPro; IPR000626; Ubiquitin.
Pfam; PF00627; UBA; 2.
Pfam; PF00240; ubiquitin; 1.
SMART; SM00165; UBA; 2.
SMART; SM00213; UBQ; 1.
SEQUENCE CO. BUSE;
STRAIN=Y, CR BW SP;
Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Lewis S., Li P., Lomotan M.A., Mazda P., Woshrefi A.R., Moshrefi N.
Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
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01-NOV-1996
01-DEC-2001
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[2]
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STRAIN-Y, CN BW SP;
MEDLINE-99403001; PubMed=10471707;
MEDLINE-99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Boyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Moshrefi A.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Hong L., Houston K., Hoskins R., Johnson G., Wan K., Whitelaw K.,
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                                                                                                                                                                                                                                                                                    Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Trachea
Pterygota; Neoptera; Endopterygota; Dip
Ephydroidea; Drosophilidae; Drosophila.
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                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryo
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eurosids II; Brassicales; Brassicaceae; Arabio
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AE003408; AAF44847.1; -.
FlyBase; Fbgn0028907; BG:DS01514.3.
Hypothetical protein.
SEQUENCE 395 AA; 43561 MW; AE4F1CC4ADD3DA7
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
T17H3.2 PROTEIN (AT1G27520/T17H3_2).
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Matches 10; Conserv
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Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AC005916; AAD45990.1; -.

EMBL; AC0055382; AAL08238.1; -.

HSSP; p32906; 1DL2.

InterPro; IPR001382; Glyco_hydro_47.

Pfam; PF01532; Glyco_hydro_47; 1.

PRINTS; PR00747; GLYHDRLASE47.

PRODOm; PD003239; Glyco_hydro_47; 1.

PRODOm; PD003239; Glyco_hydro_47; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. COLUMBIA;

Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,

Lee J.M., Liu A., Li J., Gonzalez A., Liu K., Vaysberg M., Sakano H.,

Chin C., Howng B., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,

Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,

Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M.,

Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;

"Arabidopsis thaliana chromosome 1 BAC T17H3 sequence.";

Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,

Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,

Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,

Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,

Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,

Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ecker J.R.;
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                                                                                                     3 TEQVEVPGSQHIDSQKK 19
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19 TEFVVDPSSQHIEVKKK 35
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2; Mismatches
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Gapop 10.0 , Gapext 0.5
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39
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AAY87461
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Residues 50-64 of
Sequence of amino
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                                                                     Cholera toxin B/en Cholera toxin B/en Cholera toxin B/en CTP3 epitope of th Cholera toxin B an Cholera toxin B/en E. coli heat labil
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22	22	22	22	22	22	22	22	22	21	21	19	17	10	22	22	11	22	22	22	22	22	19	17	17	17	17	σ	22	21	20	20	16	4
AAB62380	N	AAB62376	AAB62375	AAB62373	AAB62368	AAB62363	AAB62359	AAG65992	7	AAY96652	AAW59770	AAW06605	AAP93561	AAB62377	AAB62374	AAR04163	AAB62369	AAB62379	AAB62370	AAB62367	AAB62365	AAW80808	AAW06607	AAW06606	AAR94939	AAW04857	AAP50340	AAB66239	AAY68365	AAW95226	AAY41816	AAR72545	AAP30600
LTB	LTB	LTB	E. coli LTB protei	E. coli LTB protei	V. cholera cholera	V. cholera cholera	V. cholera strain	Cholera toxin B su		Plant-optimized E.	a	Cholera toxin B su	B subunit of the h	E. coli LTB protei	E. coli LTB protei	Cholera Toxin B-su	V. cholera cholera	E. coli LTB protei	V. cholera cholera			Amino acid sequenc	Cholera toxin B su	w	Heat labile entero	Synthetic cholera	Sequence of sub-un	E coli verotoxin-1	Heat labile toxin	E. coli heat-labil		\sim	Sequence of amino

ALIGNMENTS

RESULT AAY87460 IJ Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:2 03-JUL-2000 (first entry) AAY87460 standard; peptide; Williams NA, 07-SEP-1998; 07-SEP-1999; WO200014114-A1 Vibrio cholerae. Escherichia coli. adjuvant; immune Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; AAY87460; (UYBR-) UNIV BRISTOL. 16-MAR-2000. beta-4-alpha-2 loop; GM-1 ganglioside receptor; Hirst TR; 98GB-0019484 99WO-GB02970 disorder; diarrhoea. 7 ₽ immunomodulation;

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

WPI; 2000-256943/22.

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cc labile enterotoxin (Etx) and its closely related homologue, cholera ct toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous composed of one A subunit and five identical B subunits. The A subunit cc is responsible for toxicity, while the B subunits (EtxB and Ctx are ribosyltransferase activity, while the B subunits (EtxB and CtxB) cc facilitate the entry of subunit A into the host cell via the binding and cc cross-linking of GM-1 receptors. Although GM-1 binding is responsible cffects of Etx and Ctx, it has been found that certain cc fifects of the toxins, such as immunomodulation, are not mediated cc through GM-1 binding. The peptides of the invention are fragments of the course for subunits, except that they do not bind or cross link cross in the subunits, except that they do not bind or cross link cff. They may be used in medicine as an immunomodulator or adjuvant. Cc GM-1. They may be used as an inhibitor for toxin-induced diarrhoea. Cc Immune disorder and/or toxin-induced diarrhoea. Sequences AXY87460-Y87463 cc particularly preferred peptides of the invention, AAY87460 being cc particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thehes 7; Conserv
   рь
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   Example 5;
                                           Derivatives of Escherichia coll heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind {\tt t}
                                                                                                                                                                                                                                                                                                                                                                             Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 13; 62pp; English.
                                glycolipid receptor GM-1
                                                                                            WPI; 2000-256943/22.
                                                                                                                                                          (UYBR-) UNIV BRISTOL
                                                                                                                                                                                        07-SEP-1998;
                                                                                                                                                                                                                       07-SEP-1999;
                                                                                                                                                                                                                                                    16-MAR-2000
                                                                                                                                                                                                                                                                                   WO200014114-A1
                                                                                                                                                                                                                                                                                                                  Escherichia coli.
                                                                                                                                                                                                                                                                                                                                  Vibrío cholerae
                                                                                                                                                                                                                                                                                                                                                                adjuvant; immune
                                                                                                                                                                                                                                                                                                                                                                                                                          Cholera toxin B/enterotoxin B-derived immunomodulatory peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY87464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY87464 standard; peptide; 8 AA
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1 evpgsqh 7
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Page 45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                           Hirst TR;
                                                                                                                                                                                        98GB-0019484
                                                                                                                                                                                                                       99WO-GB02970
                                                                                                                                                                                                                                                                                                                                                                 disorder; diarrhoea
 62pp; English
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100.0%; Pred. No. 6.,
tive 0; Mismatches
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ches 0;
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The invention relates to peptide fragments of the Escherichia coli heat CC labile enterotoxin (Etx) and its closely related homologue, cholera coli toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit cc is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) and cross-linking of GM-1 receptors. Although GM-1 binding is responsible cross-linking of GM-1 receptors. Although GM-1 binding is responsible coross-linking of GM-1 receptors. Although GM-1 binding is responsible coross-linking of the fetx and Ctx, it has been found that certain ceffects of the toxins, such as immunomodulation, are not mediated corosments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the corosments of the beta-4-alpha-2 loop of EtxB and/or CtxB, exerting the composition of the production of a composition for treating, preventing and corosmodulator or adjuvant. They may also be used as an inhibitor for conduction of a composition for treating, preventing and/or modulating a composition of the present invention to assess whether a peptide corresponding to a portion of the beta-4-alpha-2 loop, and peptide AAY87465 is a randomly selected control perfects. Peptide AAY87464 corresponds to residues corresponds to residues beta-4-alpha-2 loop, and peptide AAY87465 is a corresponding selected control perfects.
Sequence
                                                         randomly selected control peptide.
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Query Match
Best Local Similarity
""+"hes 7; Conserv 1 EVPGSQH 7 1 evpgsqh 7 Conservative 100.0%; Score 39; DB 21; 100.0%; Pred. No. 6.4e+05; 0; Mismatches Length Indels 0 Gaps 0

RESULT AAY87461

밁 Qy

AAY87461 standard; peptide;

AAY87461;

03-JUL-2000 (first entry)

Cholera toxin B/enterotoxin B-derived peptide, SEQ Ħ NO: 3

beta-4-alpha-2 loop; GM-1 ganglioside receptor; adjuvant; immune disorder; diarrhoea. Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B; EtxB;

Vibrio cholerae. Escherichia coli

WO200014114-A1

16-MAR-2000.

07-SEP-1999; 99WO-GB02970

07-SEP-1998; 98GB-0019484

(UYBR-) UNIV BRISTOL

Williams NA, Hirst TR;

WPI; 2000-256943/22.

Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor ${\tt GM-1}$ -

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RESULT
AAP93498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cc is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CC ribosyltransferase activity, while the B subunits (EtxB and CtxB) CC facilitate the entry of subunit A into the host cell via the binding and CC cross-linking of GM-1 receptors. Although GM-1 binding is responsible CC for some of the effects of Etx and Ctx, it has been found that certain CC effects of the toxins, such as immunomodulation, are not mediated CC through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as CC normal EtxB and CtxB subunits, except that they do not bind or cross link CC GM-1. They may be used in medicine as an immunomodulator or adjuvant. CC They may also be used as an inhibitor for toxin-induced diarrhoea. CC for treating, preventing and/or modulating a disease associated with an CC control disorder and/or toxin-induced diarrhoea. Sequences Ax87460-Y87463 crepresent preferred peptides of the invention, Aay87460 being particularly preferred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit
                                                          epitope, and expressed
of antibodies:
                                                                                                                     WPI; 1989-356496/48.
N-PSDB; AAN92414.
                                                                                                                                                                                                                                           05-MAY-1988;
                                                                                                                                                                                                                                                                         05-MAY-1989;
                                                                                                                                                                                                                                                                                                                                   W08910967-A
                                                                                                                                                                                                                                                                                                                                                                           CTP3 epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                   New recombinant flagellin gene including sequence epitope, and expressed fusion proteins, useful in
                                                                                                                                                                 Marjarian WR,
                                                                                                                                                                                                                                                                                                       16-NOV-1989
                                                                                                                                                                                                                                                                                                                                                              vaccine; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAY-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP93498 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                              (PRAX-) PRAXIS BIOLOGICS INC (STRD ) LEYLAND STANDFORD JUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                              of Cholera
                                                                                                                                                                                                                                                                                                                                                                                                            of the Cholera
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                                                                                                                                                                                                                                           88US-0190570
                                                                                                                                                                                                                                                                         89WO-US01932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62pp; English.
                                                                                                                                                                 BAD,
                                                                                                                                                                                                                                                                                                                                                                ds;
                                                                                                                                                                                                                                                                                                                                                                              toxin B subunit; flagellin fusion protein;
                                                                                                                                                                                               JUNIOR UNIV.
                                                                                                                                                                                                                                                                                                                                                                                                          toxin B subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 39; DB Pred. No. 0.2 0; Mismatches
                                                                                                                                                                 Newton
                                                                                                                                                                 SMC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2:
0.29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 12;

    for heterologous 
vaccines and for prodn

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli heat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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This sequence corresponds to the CTP3 epitope of the Cholera toxin

Disclosure; fig.4B; 137pp; English.

Query Match
Best Local Similarity
"-+-hes 7; Consery:

100. nilarity 100. Conservative

.0%;

Score 39; Pred. No.

0.37; DB 16;

Length 15;

0;

Mismatches

0;

Indels

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Gaps

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1 EVPGSQH

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AAR85125
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         subunit. The DNA sequence encoding this ligates to othersynthetic oligonuclectides to form a new recombinant gene. This encodes a flagellin fusion protein which can be used in vaccines for immur therapy.
                                     A compsn. comprising a conjugate of an antigenic cholera B toxin peptide fragment (e.g. AAR85126-30 and esp. AAR85125), covalently bound to a microparticulate inert carrier (e.g. modified silica c thyroglobulin) can be used as an oral vaccine for immunisation against cholera infection. The inert carrier is insoluble in the digestive tract, allowing presentation of the antigen in the intestines, where it will elicit antibodies mainly of the
                                                                                                                                                                                      Vaccines for oral immunisation against infecting agents, e.g. cholera - comprise a conjugate of an antigen of an infecting agent covalently bound to micro:particulate inert carrier, e.g. modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                        03-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cholera toxin B antigenic peptide fragment CTP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR85125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR85125 standard; peptide; 15
Sequence
                           secretory
                                                                                                                                               Claim 7; Page 25; 40pp;
                                                                                                                                                                                                                                                                    Marks RS,
                                                                                                                                                                                                                                                                                             (YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                  02-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                             09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                      W09529701-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                          intestines; antibodies; secretory; IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inert carrier; modified silica; thyroglobulin; oral vaccine;
immunisation; infection; insoluble; digestive tract; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conjugate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EVPGSQH 7
|||||||
2 evpgsqh 8
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                                                                                                                                                                                                                                          1995-403805/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 7; Conserv
                                                                                                                                                                           silica
                                                                                                                                                                                                                                                                    Mirelman D,
                          IgA class.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cholera;
15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified silica;
                                                                                                                                                                                                                                                                                                                        94IL-0109519
                                                                                                                                                                                                                                                                                                                                                 95WO-EP01661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B toxin; peptide fragment; microparticulate; fied silica; thyroglobulin; oral vaccine;
                                                                                                                                               English.
                                                                                                                                                                                                                                                                    Sela M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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                                                                                                        covalently
                                                                                             silica or
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evpgsqh

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Query Match
Best Local Similarity
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AAY87462
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                                                                                                                                                                                   effects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as normal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea. Therefore, the peptides may be used in the production of a composition for treating, preventing and/or modulating a disease associated with an immune disorder and/or toxin-induced diarrhoea. Sequences AAX87460-Y87463 represent preferred peptides of the invention, AAY87460 being particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                               The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholera which do not bind to the ubiquitous GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit is responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-facilitate the entry of subunit the B subunits (EtxB and CtxB) facilitate the entry of subunit A into the host cell via the binding and cross-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain
                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycolipid receptor GM-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-256943/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cholera toxin subunit B; CtxB; heat labile enterotoxin subunit B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY87462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY87462 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200014114-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cholera toxin B/enterotoxin B-derived peptide, SEQ ID NO:4.
 7
                                  1 EVPGSQH 7
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evpgsqh 13
                                                                                                                                                       21
                                                                      Conservative
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                                                                                                                                                       ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0019484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB02970.
                                                                                   100.0%;
                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                   Score 39;
Pred. No.
                                                                      Mismatches
                                                                                   0.52;
                                                                                                 DB 21;
                                                                    0;
                                                                                                 Length 21;
                                                                    Indels
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RESULT AAR76748

Db δÃ

7 evpgsqh 13

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RESULT
AAY87463
                                                                                                                                                                                                                                                                     CC GM-1 ganglioside receptors on host cell surfaces. Both Etx and Ctx are composed of one A subunit and five identical B subunits. The A subunit cis responsible for toxicity, possessing adenosine diphosphate (ADP) ADP-CT ribosyltransferase activity, while the B subunits (EtxB and CtxB) across-linking of GM-1 receptors. Although GM-1 binding is responsible for some of the effects of Etx and Ctx, it has been found that certain ceffects of the toxins, such as immunomodulation, are not mediated through GM-1 binding. The peptides of the invention are fragments of the beta-4- alpha-2 loop of EtxB and/or CtxB, exerting the same effects as cormal EtxB and CtxB subunits, except that they do not bind or cross link GM-1. They may be used in medicine as an immunomodulator or adjuvant. They may also be used as an inhibitor for toxin-induced diarrhoea.

Therefore, the peptides may be used in the production of a composition of immune disorder and/or toxin-induced diarrhoea. Sequences AAY87460-Y87463 represent preferred peptides of the invention, AAY87460 being
                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to peptide fragments of the Escherichia coli heat labile enterotoxin (Etx) and its closely related homologue, cholera toxin (Ctx) from Vibrio cholerae which do not bind to the ubiquitous
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                         particularly preferred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 15; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            glycolipid receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Derivatives of Escherichia coli heat labile enterotoxins useful as immunomodulators and for treating diarrhea and which do not bind the glycolipid receptor GM-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-256943/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Williams NA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heat labile enterotoxin subunit B; EtxB; beta-4-alpha-2 loop; GM-1 ganglioside receptor; immunomodulation; adjuvant; immune disorder; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYBR-) UNIV BRISTOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200014114-A1
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1 EVPGSQH 7
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                                                                                                                                                                                                    21 AA;
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirst TR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               labile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterotoxin
                                                                               100.0%;
                                                          0;
                                                                                  Score 39; DB 2
Pred. No. 0.52;
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-derived
                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide,
                                                          0;
                                                                                                               Length 21; /
                                                       Indels
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                                                          0;
                                                          Gaps
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                                                                               This sequence is encoded by a fragment of the the plasmid pLPA93

CC which was used in the production of finh fusion genes comprising

Ct the cholera toxin B subunit inserted into the finh gene. This insert

CC shows the inclusion of the B subunit into the finh protein at position

CC 224-226. The chimeric genes were then opt. further modified by insertion

CC of the hepatitis B virus surface antigen pre-S2 region into a different

CC cosition of the Finh adhesin of type 1 fimbriae. Restletion site handles

CC (BglII-sites) were introduced into the finh gene, and the foreign

CC epitopes are then inserted in-frame. In the selected positions the

CC insertion of the epitopes did not significantly alter the adhesive

CC of unction of the Finh protein. The expression of the chimeric proteins

CC on the surface of finbriae on bacterial hosts illustrated the possibility

CC of using bacterial adhesins as general presenters of foreign antigens and

CC epitopes. These chimeric genes may be used in the production of variant

CC Finh adhesins which may be useful for targetting active compounds
                             Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FimH;
FimA;
                                                                                                                                                                                                                                                                                                        Receptor specific bacterial adhesins - useful for targetting active compounds and microbial cells to locations of receptors
                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAQ93061
                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-275442/36
                                                                                                                                                                                                                                                                                                                                                                    Hasty
                                                                                                                                                                                                                                                                                                                                                                                                             27-JAN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                27-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9520657-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                               Sequence
                                                                                                             and microbial cells
                                                                                                                                                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR76748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR76748 standard; Protein; 23 AA.
                                                                                                                                                                                                                                                                                                                                                                                         (GXBI-) GX BIOSYSTEMS
                             Local Similarity
mes 7; Conser
          1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                     DL,
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                                                                                                                                                                                                                                                                                    3; Page 58; 152pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50-64 of
                                                                                                                                                                                                                                                                                                                                                                    Klemm P,
                                                                                23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 fimbriae; organelle; adhesin; alpha-D-mannoside residue;
; FimG; receptor binding site; PCR; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                             94US-0187166
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23
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20..22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Linker peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Represents FimH residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Linker peptide"
                                       . 0%;
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Guyongruaz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be administrated by the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CNRS
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                                                                                                                                                AAP50439 standard; protein; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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2 evpgsqh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conserv
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Pred. No. 0.65;
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Network polymer which comprises a series of composite E. coli heat-labile toxin (LT)/heat-stable toxin (ST) polypeptide repeating untis.

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Best Local S
Matches 7
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                                                                                                                                                                                                                           01-JAN-1980
         WPI; 1985-159230/26
                            Houghten RA;
                                                                                                                                 WO8502611-A.
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                                                                      12-DEC-1983;
                                                                                          12-DEC-1984;
                                                                                                              20-JUN-1985
                                                                                                                                                     Synthetic
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                                                 (SCRI-) SCRIPPS
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7; Conserv
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Pred. No.
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AAP50439-57.
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                                                           The inventors claim cholera toxin B1 subunit sequences which carry Arg in posn. 35, 67 or 73 (AAP30264, AAP30265, AAP30600). Tests have shown that Arg in posns. 35, 67 and 73 play an important role in fixing these toxins to cell walls. The peptides are used in the treatment of, and vaccination against, cholera infections and animal and human infections due to E. coli (enterotoxin LT). The medicament may be
                                                                                                                                                                                    Cholera toxin B, sub-unit polypeptide(s) as vaccines and medicaments - effective against Escherichia coli and Vibrio cholerae infections, are prepd. by solid phase peptide syntlements.
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                       administered by oral, intraperitoneal, sub-cutaneous or intravenous routes. For vaccines, pref. peptides having 15-30 AAs are injected without carriers. Unit dose when used as a medicament is 50-500mg a
                                                                                                                                                          Claim 8; Page 11; 13pp; French.
                                                                                                                                                                                                                                                                    Guyongruaz A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cholera vaccine;
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                                                                                                                                                                                                                                                                                   Milhaud
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A, Delmas A;
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Best Local S
Matches 7
                                                                             Query Match
Best Local
                                                                      Matches
                                                                                                                                                 AAR72540-R72545 are structurally equivalent B-subunits from three ADP-ribosylating toxins, pertussis holotoxtin (FT), E. Coli heat labile toxin (LT), and verotoxin-1 (VT). The structural information obtd. from these comparisons was used to identify sites which contribute to FT's biological activity. By modifying these sites the claimed PT mutants of the invention were produced, they can be used in the development of vaccines against Bordetella
                                                                                                                                                                                                                                                     New modified forms of pertussis holotoxin - crystalline forms of pertussis holotoxin and other molecules
                                                                                                                                                                                                                                 Disclosure; Fig 5; 54pp; English.
                                                                                                                                                                                                                                                                                            WPI; 1995-132623/18.
                                                                                                                                                                                                                                                                                                               Armstrong GD,
Oomen R, Read
                                                                                                                                                                                                                                                                                                                                                                          24-AUG-1993;
31-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EP646599-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADP-ribosylating toxin; pertussis holotoxin; B-subunit; active site; E. coli heat labile toxin; verotoxin-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP-ribosylating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR72545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR72545 standard; peptide; 93 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-NOV-1995
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                                                 1 EVPGSQH 7
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| evpgsqh
                            evpgsqh
                                                                   Similarity 7; Conserv
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                                                                                                                                         infection
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                                                                                                                     93
                                                                     Conservative
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RJ, Stein
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94US-0251121.
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tive 0;
                                                                             100.0%;
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                                                                                                                                                                                                                                                                                                                 Hazes PE;
                                                                    0;
                                                                             Score 39; Pred. No.
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Pred. No.
                                                                    Mismatches
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                                                                                       Length
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                                                                    Indels
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                                                                            QΥ
Χij
                                                          В
                   AAW95226
                              RESULT
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RESULT

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AAW95226 standard; peptide; 93

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Query Match
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                                                                                                                                                                                                    A method has been developed of producing a modified pertussis holotoxin, convolving analysis of the 3-dimensional form of the crystalline cholotoxin. The pertussis holotoxin modification process comprises:

CC (1) identification of at least one amino acid (aa) residue of the cholotoxin for modification by analysing the 3-dimensional form of the crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein crystalline holotoxin, in relation to known information of the protein crystalline and clocking a nucleotide sequence encoding at least one (aa)) of a tox operon; and (3) expressing mutant tox box in a Bordetella organism to produce the modified holotoxin. This method is used for modifying contribusing the holotoxin, alters its biological properties.

CC produce the modifying the holotoxin, alters its biological properties.

CC proture. Modifying the holotoxin, alters its biological properties.

CC blotoxin, functional (aa) which affect biological properties of the pertussis holotoxin can be identified. This can be used to predict (aa) which contribute to the toxicity of the holotoxin to produce immunoprotective, genetically-detoxified analogues of pertussis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
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Hazes B,
                                                                                                                                  Sequence
                                                                                                                                                                             holotoxin. The present sequence represents an ADP-ribosylating toxin B-subunit peptide used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New method for producing modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADP-ribosylating toxin; PT; crystalline pertussis holotoxin; ETA; three-dimensional structure; LT; immunoprotective; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
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evpgsqh
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93US-0110947.
94US-0251121.
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                                                                         Score 39;
Pred. No.
                                                             Mismatches
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                                                                                                                                                                                                                                              The invention relates to methods of preparing a pertussis holotoxin (PT) CC having a modified biological activity. One method comprises identifying CC at least 1 site in a PT that interacts with a molecule that is capable of CC forming a complex with the holotoxin and which molecule is an effector CC molecule which is an adenine nucleotide and which site contributes to CC toxicity, cell binding or enzymatic activity of PT. The functional CC interacting site(s) are identified by analysing the three dimensional CC identified interacting site(s) are modified to alter toxicity, cell cidentified interacting site(s) are modified to alter toxicity, cell coilogical activity such as toxicity, enzymatic activity, mitogenicity, CC cell binding and adjuvanticity of the PT. The methods can be used to alter a CC toxins such as diphtheria toxin (DT), Pseudomonas exotoxin A (ETA), the CC heat-labile toxin of E. coli (LT) and verotoxin-1 (VT). The present cover contributes the beta-subunit of LT toxin.
                                                                                                                                         Query Match
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Matches 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1994;
24-AUG-1993;
31-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pertussis holotoxin; PT; modified; effector; toxicity; cell binding; enzyme; ADP-ribosylation; toxin; crystalline; X-ray crystallography; structural analysis; interacting site; mitogenicity; adjuvanticity; heat-labile; LT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modifications to e.g. enzymatic activity, mitogenicity and cell binding of pertussin holotoxin - by identifying interaction sites of a molecule with crystalline toxin and modifying the identified site
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Oomen RP, Read
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                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 5; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-105104/09.
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93US-0110947.
94US-0251121.
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Pred. No. 2.4
); Mismatches
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                                                                                                                                                        2.4;
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                                                                                                                                                                      Length 93;
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Title:
Perfect score:
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Maximum Match 100%
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
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3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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length: 2000000000
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US-09-082-514-26
US-08-952-337-5
US-08-952-337-6
US-08-952-337-6
US-09-913-047-2
US-09-913-047-2
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Sequence 34, Appl	Sequence 4, Appli	Sequence 48, Appl	Sequence 48, Appl	Sequence 62, Appl	Sequence 3, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Patent No. 5194375	Sequence 8, Appli	Sequence 8, Appli	Sequence 8, Appli

ALIGNMENTS

RESULT

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US-08-467-974-26
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                                                                                                                                                                                                                                                            PILING DATE: 22-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/251,121
FILING DATE: 31-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947

FILING DATE: 24-AUG-1993

ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.

PRIOR APPLICATION NUMBER: 24-AUG-1993
                                                                                                                                                                          TELEFAX: (416) 595-116
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 1038-454 MIS:vg
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
APPLICANT: HAZES, Bart
TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE: 06-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Suite CITY: Toronto STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/467,974 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 EVPGSQH 47
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            Score 39; DB 2; Length 93; Pred. No. 0.67; Indels
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Pred. No. 0.67;
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GENERAL INFORMATION:
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APPLICANT:
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APPLICANT:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                       41 EVPGSQH 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 06-JUN CLASSIFICATION: 435
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41 EVPGSQH 47
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ZIP: M5G 1R7
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TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 26
                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0: FILING DATE: 31-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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Suite 701, 330 University Avenue
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 Conservative
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06-JUN-1995
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100.0%; Score 39; DB 2;
100.0%; Pred. No. 0.67;
Live 0; Mismatches 0
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                                   Length 93;
   Indels
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Sequence Patent No.

26,

Application US/08467976

GENERAL

INFORMATION:

APPLICANT: APPLICANT:

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US-09-082-514-26

; Sequence 26, Application US/09082514

; Patent No. 6168928
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Best Local Similarity
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                                                                            GENERAL INFORMATION:
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                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0 FILING DATE: 31-MAY-1994 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/292,968
FILING DATE: 22-AUG-1994
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
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                                                                                                                                                                                                                         1 EVPGSQH 7
                                                                                                                                                                                           EVPGSQH 47
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M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SSEE: Sim & McBurney
T: Suite 701, 330 University Avenue
Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STEWART, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ontario
STEIN, Penelope E. COCKLE, Stephen A. OOMEN, Raymond P. KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           READ, Randy J.
STEIN, Penelope E.
COCKLE, Stephen A.
OOMEN, Raymond P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAZES, Bart
                                                             READ, Randy J.
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOOSMORE,
                                                                                                                                                                                                                                                                                                                                                    linear
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                                                                                                                                                                                                                                                                    Score 39; DB 3
Pred. No. 0.67;
                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                   Length 93
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; ORGANISM: Vibrio cholerae
US-08-952-337-5
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                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 5
LENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08952337 Patent No. 6019973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 39; DB 4 Best Local Similarity 100.0%; Pred. No. 0.67; Matches 7; Conservative 0; Mismatches
                                                                                                                                                      CURRENT APPLICATION NUMBER: US/08/952,337 CURRENT FILING DATE: 1998-01-05 EARLIER APPLICATION NUMBER: PCT/SE96/00570 EARLIER FILING DATE: 1996-05-02 EARLIER APPLICATION NUMBER: SE 9501682-0
                                                                                                                                                                                                                                      APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D/58
CURRENT APPLICATION NUMBER: US/08/952,337
                                                                                                                                    EARLIER FILING DATE: 1995-05-05
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER:
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ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MODIFICATION OF PERTUSSIS TOXIN NUMBER OF SEQUENCES: 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDATE OUT.
STREET: OUT.
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HAZES, Bart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                Windows Version 3.0
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Best Local Similarity
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Best Local Similarity
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US-08-472-171-2
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; ORGANISM: Escherichia coli
US-08-952-337-6
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                              COUNTRY: Canada
ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,171
ETLING DATE: 07-JUN-1995
CLASSIFICATION: 435
DEFICE ADDITION TO A APPLICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08472171 Patent No. 5932714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTERROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D78
FULRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LOOSMORE, Sheena
APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
                                                                                                                                                                                                                                                          STREET: 330 Ur
CITY: Toronto
STATE: Ontario
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                            330 University Avenue, Suite 701
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                                                                                                                                                                                                                                                                                                                   Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                        Expression Of Gene Products From Genetically Manipulated Strains Of Bordetella
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US 08/393,334
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; TOPOLOGY: 1; MOLECULE TYPE: US-08-894-526-2
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Best Local Similarity
7; Conserva
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                                                                                                                                        COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/894,526
FILING DATE: 01-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 1038-724 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2,
                                                                                     TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EXPRESSION OF GENE PRODUCTS FROM
TITLE OF INVENTION: GENETICALLY MANIPULATED STRAINS OF BORDETELLA
NUMBER OF SEQUENCES: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 416-595-1155
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ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 1038-507 MIS:vg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
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M5G 1R7
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                                                      amino acid
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                                                                       103 amino acids
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Zealey, Gavin R
Klein, Michel H
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Query Match Best Local Similarity

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Score 39; DB 2; Pred. No. 0.74;

Length 103;

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Query Match
Best. Local Similarity
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                                                          RESULT 11
US-09-374-597-2
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US-09-013-047-2
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Sequence 2, Application Patent No. 6140082 GENERAL INFORMATION: APPLICANT: LOOSMOTE,
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                                                                                                                                                                                                                                                                                                      TELEFAX: 416-595-1163
TELEX: 065-24567 Simbas
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/472,171
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,334
FILING DATE: 23-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Ontario
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                                                                                                                                                1 EVPGSQH 7
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| EVPGSQH 57
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                                                                                                                                                                                                                                                                                           amino acid
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Stewart, Michael I.

---- MIMBER: 24,973
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Loosmore, Sheena M.
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                                          US/09374597
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CURRENT APPLICATION DATA:
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RESULT 12
US-09-191-852-21
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Patent No. 6194560
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Best Local
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                        TITLE OF INVENTION: OF NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                            NERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, and Tariq A. Haq
APPLICANT: Charles J. Arntzen Hugh S. Mason, and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
NUMBER OF SEQUENCES: 56
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APPLICATION NUMBER:
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ADDRESSEE: Sim & McBurney
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51 EVPGSQH 57
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TELEX: 065-24567 Simbas
TELEX: 065-1163
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                                                                                                  COUNTRY: UZIP: 77010
                                                                                                                                     STATE:
                                                                                                                                                       CITY: Houston
                                                                                                                                                                      STREET:
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1301 McKinney, Suite 5100
                                                                                                                   USA
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ilarity 100.0%;
Conservative (
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Pred. No. 0.74;
Mismatches
 Version #1.25
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; TOPOLOGY:
PCT-US95-13376-21
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PCT-US95-13376-21
Sequence 21, Application PC/TUS9513376
GENERAL INFORMATION:
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                                                                                             TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 21:
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INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13376
                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acid
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REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: PO:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                   REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 24-OCT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The Texas A&M University System
APPLICANT: 310 Wisenbaker
APPLICANT: College Station, Texas 77843-3369
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
NUMBER OF SEQUENCES: 23
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APPLICATION NUMBER: PCT/US95/13376
FILING DATE: 24 - OCT - 1995
APPLICATION NUMBER: 08/817,906
FILING DATE: 04-AUG-1997
ATTORNEY/AGENT INFORMATION:
NAME: FCY PAYOR INFORMATION:
                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                            NAME: Jones, John W. REGISTRATION NUMBER: 31,380
                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 77027-9095
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                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                      amino acid
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1177 West Loop South, 10th Floor
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                    linear
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Pred. No. 0.74;
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; TYPE: PRT ; ORGANISM: Eschcerichia US-08-952-337-2
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US-08-952-337-1
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SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 123
TYPE: PRT
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SOFTWARE: FRASTSEQ for Windows Version
SEQ ID NO 2
LENGTH: 123
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APPLICANT: Holmgren, Jan
APPLICANT: Lebens, Michael R.
APPLICANT: Lebens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTERCTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                      APPLICANT: Holmgren, Jan
APPLICANT: Holmgren, Jan
APPLICANT: Labens, Michael R.
TITLE OF INVENTION: HYBRID MOLECULES BETWEEEN HEAT-LABILE
TITLE OF INVENTION: ENTEROTOXIN AND CHOLERA TOXIN B SUBUNITS
FILE REFERENCE: 3846/0D758
CURRENT APPLICATION NUMBER: US/08/952,337
CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER APPLICATION NUMBER: SE 9501682-0
EARLIER FILING DATE: 1995-05-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08952337 Patent No. 6019973
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CURRENT FILING DATE: 1998-01-05
EARLIER APPLICATION NUMBER: PCT/SE96/00570
EARLIER FILING DATE: 1996-05-02
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100.0%; Score 39; DB ilarity 100.0%; Pred. No. 0.9; Conservative 0; Mismatches
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Pred. No. 0.
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                                      DB 3;
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Indels

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Qy 1 EVPGSQH 7
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Db 71 EVPGSQH 77

Search completed: July 3, 2002, 08:55:38
Job time: 213 sec

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Minimum
Maximum
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Copyright (c) 1993 - 2000 Comp
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1 US-09-786-648-3

1 US-08-732-371A-1

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1 US-09-786-648-4

1 US-09-786-648-5

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ALIGNMENTS	09-402-532-	-US01-08582-	-US01-085	-09-402-532-	S-09-402-532-1	09-489-847-3	-US99-17130-	60-171-481-1	09-760-234-	US-09-866-066-35	PCT-US01-08631-54035	PCT-US01-08631-32551	PCT-US01-08631-32459	PCT-US01-08631-32869	US-09-417-507-29272	09-617-682A-	US-09-688-051-2967	US-60-361-742-1547	US-08-829-026-5	-80-	A-3	-09-756-983-2	US-09-756-983-18	-09-756-983-1	-08-914-479A-	-08-914-479-2	S-09-470-124-	09-470-124-5	in i	TS99-30747-5	09-836-433-2	S-09-836-433-2	S-09-836-433-1	s-08-817-906-	S-08-782-832-1	-08-393-334-2	-08-251-121-26	US-08-110-947A-26
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ALIGNMENTS

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; FEATURE:
; LOCATION: 51...57
; OTHER INFORMATION: isolated or synthetic EtxB beta4-alpha2 loop fragment derivabl
; OTHER INFORMATION: human variant E. coli
US-09-786-648-2
Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-786-648-2
                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
PRIOR FILING DATE: 1999-09-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: MS DOS
SEQ ID NO 2
LENGTH: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09786648 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vacci
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: E.
                                                                                                                                                                                                                                   coli
                                      100.0%;
               Score 39; DB Z1;
Pred. No. 3.2e+06;
                                                        Length 7;
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Conservative

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Indels

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Gaps

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                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/732,371
FILING DATE: 09-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: IL 109519
APPLICATION NUMBER: IL 109519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Peptide Fragments TITLE OF INVENTION: Adjuvants FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Williams, Neil Andrew APPLICANT: Hirst, Timothy Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6 SOFTWARE: MS DOS
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OTHER INFORMATION:
OTHER INFORMATION:
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FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                    FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MIRELMAN, David
APPLICANT: MARKS, Robert S.
APPLICANT: SELA, Michael
TITLE OF INVENTION: VACCINE;
TITLE OF INVENTION: INFECTII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENGTH: 12
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                 NAME: YUN, Allen C. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                   ZIP: 20004
                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                           419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                      USA
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NUMBER: MIRELMAN=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VACCINES FOR ORAL IMMUNIZATION AGAINST INFECTING AGENTS
                   37,971
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Pred. No. 2.4;
D; Mismatches
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Best Local Similarity
Thes 7; Conserve
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GENERAL INFORMATION:
Best Local Similarity
Matches 7; Conserv
 Matches
                             Query Match
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                 TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 10
FILING DATE: 03-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 09-JAN-199
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: VACCINES FOR ORAL IMMUNIZATION AGAINST TITLE OF INVENTION: INFECTING AGENTS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                        TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                           REGISTRATION NUMBER: 37 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 15 amino acids TYPE: amino acid
                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                     YUN, Allen C.
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419 Seventh Street, N.W., Suite 300
                                                                                                                                  15 amino acids
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SELA, Michael
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MARKS, Robert S.
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 Conservative
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                                                                                       protein
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               Score 39; DB Pred. No. 3.1;
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 Mismatches
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                             DB 11; Length 15;
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COTHER INFORMATION:
COTHER INFORMATION:
US-09-786-648-5
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GENERAL INFORMATION:
APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09786648 GENERAL INFORMATION:
                                                                                      Query Match
Best Local
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Best Local 9
                                                                     Matches
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SEQ ID NO 5
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                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/786,648
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: PCT/GB99/02970
PRIOR FILING DATE: 1999-09-07
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin B as Vaccine
TITLE OF INVENTION: Adjuvants
FILE REFERENCE: 7438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Williams, Neil Andrew
APPLICANT: Hirst, Timothy Raymond
TITLE OF INVENTION: Peptide Fragments of Cholera Toxin B or Enterotoxin
TITLE OF INVENTION: Adjuvants
                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 6
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SOFTWARE: MS DOS
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PRIOR APPLICATION NUMBER: PCT/GB99/02970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/786,648 CURRENT FILING DATE: 2001-03-07
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                          ORGANISM: E. coli
                                                                                                                                                                                                                                                             TYPE: PRT
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les 7; Conserv
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les 7; Conserv
                                  1 EVPGSQH 7
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                                                                     Conservative
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                                                                                                                                                                      isolated or synthetic {\tt EtxB} beta4-alpha2 loop fragment derivable porcine {\tt E.} coli
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Pred. No.
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Pred. No.
                                                                     Mismatches
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Best Local Similarity
Thes 7; Conserve
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                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 10 TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
COMPUTER READABLE FORM:
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                  TITLE OF INVENTION: MODIFICATION OF NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                  APPLICANT:
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                                                                            ADDRESSEE: Shoemaker and Mattare, Ltd.
STREET: Suite 1203 Crystal Plaza I, 2001 Jefferson
STREET: Davis Highway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Shoemaker and Mattare, Lt STREET: Suite 1203 Crystal Plaza I, STREET: Davis Hwy.
                               COUNTRY:
                                                CITY: Arlington STATE: Virginia
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REGISTRATION NUMBER: 28,946
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COCKLE, Stephen A
OOMEN, Raymond P
KLEIN, Michel H
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COCKLE, Stephen A
COMEN, Raymond P
KLEIN, Michel H
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Mismatches
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US-08-251-121-26

: Sequence 26, Application US/08251121

: GENERAL INFORMATION:
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Best Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/110,947
FILING DATE: 24-AUG-193
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
                                                                                                                                                                                                                                                                                                                           STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: READ, Randy J.
APPLICANT: STEIN, Penelope E.
APPLICANT: COCKLE, Stephen A.
APPLICANT: OOMEN, Raymond P.
APPLICANT: KLEIN, Michel H.
APPLICANT: ARMSTRONG, Glen D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (703) 415-0810
TELEFAX: (703) 415-0813
TELEX: 89-9456 LUKPAT
INFORMATION FOR SEQ ID NO: 26:
                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 28,946
REFERENCE/DOCKET NUMBER: 1038-303 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 415-0810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 93 amino acids
TYPE: amino acid
STRANDEDNESS: single
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FILING DATE: 24-AUG-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                               APPLICATION NUMBER: US/08/251,121 FILING DATE: 31-MAY-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAZES, Bart
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Pred. No. 21;
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Best Local Similarity
Thes 7; Conserve
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                                                         Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 93 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                       TELEX: 065-24567 Simbas INFORMATION FOR SEQ ID NO: :
                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: 416-595-1155
TELEFAX: 416-595-1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/393,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McB
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Yacoob, Reza K.
APPLICANT: Zealey, Gavin R.
APPLICANT: Zealey, Gavin R.
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: Expression Of Gene Products From
TITLE OF INVENTION: Genetically Manipulated Strains Of Bordetella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC PY UNIX POPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release ""
51 EVPGSQH 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                             1 EVPGSQH 7
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M5G 1R7
                                                                                                                                                                                         amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330 University Avenue, Suite 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Loosmore, Sheena M.
                                                              Conservative
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 Mismatches

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Pred. No.
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Pred. No. 23;
                                                              Mismatches
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RESULT 11 US-08-782-832-15

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                                                                                                                                                                                                                                                                 Sequence 21, Application US/08817906
GENERAL INFORMATION:
APPLICANT: Charles J. Arntzen, Hugh S. Mason, John D. Clements,
APPLICANT: and Tariq A. Haq
TITLE OF INVENTION: ORAL IMMUNIZATION WITH TRANSGENIC PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/782,832
FILING DATE: 13-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/328,716
FILING DATE: 24-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Kettelberger, Denise M.
REGISTRATION NUMBER: 33,924
REGISTRATION NUMBER: 33,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                        COMPUTER READABLE FORM:
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LENGTH: 103 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PRODUCTION OF AN ORALLY IMMUNOGENIC TITLE OF INVENTION: BACTERIAL PROTEIN IN TRANSGENIC PLAN NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                        STREET: 1301 r
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 33,924 REFERENCE/DOCKET NUMBER: 36
                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                 ADDRESSEE:
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77027-9095
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                  APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                              1301 McKinney, Suite 5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pravel, Hewitt, Kimball & Krieger 1177 West Loop South, 10th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haq, Tariq A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         713-850-0165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arntzen,
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SYSTEM: PC-DOS/MS-DOS
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US/08/817,906
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Pred. No.
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23;
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US-09-836-433-20
; Sequence 20, Application US/09836433
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENCTH: 103
TYPE: PRT
         NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin version 3.0
SEQ ID NO 20
LENGTH: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                        CURRENT APPLICATION NUMBER: US/09/836,433 CURRENT FILING DATE: 2001-04-16
                                                                                                                      APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/836,433 CURRENT FILING DATE: 2001-04-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE: Not Assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Udaka, Shigezo
TITLE OF INVENTION: HYBRID PROTEINS FOR AUTOIMMUNE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yuki, Yoshikazu
APPLICANT: Udaka, Shigezo
                                                                                                         FILE REFERENCE: Not Assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 713-651-5246
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FOX, David L.
REGISTRATION NUMBER: 40,612
REFERENCE/DOCKET NUMBER: 36:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-651-5151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 24-OCT-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                     51 EVPGSQH 57
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ORGANISM: synthetic construct

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Ouery Match
Best Local Similarity 100.0%; Score 39; DB 22; Length 116;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 EVPGSOH 7

Db 51 EVPGSOH 57

RESULT 15
US-09-836-433-22
Sequence 22, Application US/09836433
GENERAL INFORMATION:
APPLICANT: Vok.1, Yoshikazu
APPLICANT: Udaka. Shigezo
TITLE FINNERTION: HIBRID PROTEINS FOR AUTOINMUNE DISEASE
FILE REFERENCE: Not Assigned US/09/836,433
CURRENT FILING DATE: 2001-04-16
SUMMER OF SEQ ID NOS: 49
SOSTWARE: Patentin version 3.0
LENGTH: 119
TYPE: PRT
ORGANISM: Synthetic construct
US-09-836-433-22

OUETY Match
Best Local Similarity 100.0%; Score 39; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OUETY Match
SIMILARITY 100.0%; Score 39; DB 22; Length 119;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OUETY Match
SIMILARITY 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OUETY Match 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OUETY Match 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OUETY Match 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OUETY Match 100.0%; Pred. No. 27;
Matches 620 sec 0;

OUETY Match 100.0%; Pred. No. 27;
Matches 620 sec 0;

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Matches 620 sec 0;

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Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/2/paa/P

2: /cgn2_6/ptodata/2/paa/U

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4: /cgn2_6/ptodata/2/paa/U

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/cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
/cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
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US-10-110-364-8
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ALIGNMENTS

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RESULT 1

US-10-110-364-B
US-10-110-364-B
Sequence 8, Application US/10110364
Sequence 8, Application US/10110364
Sequence 8, Application US/10110364
GENERAL INFORMATION:
APPLICANY: Handley, Harold H.
APPLICANY: Bealt, Karla L.
APPLICANY: Ewalt, Karla L.
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
TITLE OF INVENTION: NUMBER: US/20/110,364
CURRENT PRILING DATE: 2000-10-05
FRIOR FILLING DATE: 2000-10-05
PRIOR FILLING DATE: 2000-10-05
PRIOR FILLING DATE: 1999-10-08
NUMBER OF SED ID NOS: 31
SOFTWARE: RESTEED FOR WINDER: 60/158,561
PRIOR FILLING DATE: 1999-10-08
NUMBER OF SED ID NOS: 31
SOFTWARE: RESTEED FOR WINDER: 60/158,561
PRIOR FILLING DATE: 1999-10-08
NEE/NOTE: 103
TYPE: PRT
ORGANISM: VIDIO Cholera
FEATURE:
NAME/KEY: VARIANT
ORGANISM: VIDIO Cholera
FEATURE:
PART ORGANISM: VIDIO Cholera
FEATURE:
NAME/KEY: VARIANT
OUGATION: (1): (103)
OTHER INFORMATION: CTB VARIANT FROM NCBI gene bank GI: 998409
US-10-110-364-8

OUS-10-110-364-8

OUS-10-110-364-8

OUS-10-110-364-10
Sequence 10, Application US/10110364
GENERAL INFORMATION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REPERENCE: ACTBIO.0044
CURRENT APPLICATION UNUMBER: US/10/110,364

CURRENT APPLICATION UNUMBER: US/10/110,364

CURRENT APPLICATION UNUMBER: US/10/110,364
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; NAME/KEY: VARIANT ; LOCATION: (1)...(103) ; LOCATION: (1)...(103) ; OTHER INFORMATION: CTB variant from NCBI gene bank GI: 14215235 ; OTHER INFORMATION: (Ogawa 41 R35D). US-10-110-364-13
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                                                                                         US-10-110-364-22
                                                                                                                RESULT
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Sequence 22, Application US/10110364
GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haapparanta, Tapio
APPLICANT: Ewalt, Karla L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 103
                                                                                                                                                                                                                                     Best Local Similarity Matches 7; Conserv
                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 13 LENGTH: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/10110364 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Handley, Harold H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 103
TYPE: PRT
ORGANISM: Vibrio cholera
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Vibrio cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                 1 EVPGSQH 7
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51 EVPGSQH 57
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                                                                                                                                                                   57
                                                                                                                                                                                                                                                        100.0%;
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Pred. No. 0.79;
                                                                                                                                                                                                                                                        Score 39; DB 6
Pred. No. 0.79;
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APPLICANT: HABDATENTA, TAPIO
APPLICANT: EWAIT, KATIB L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR ETLING DATE: 1909-10-08
NUMBER OF SEO ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
    밁
                                                                                                                                                                        ; NAME/KEY: VARIANT; LOCATION: (1)...(105); LOCATION: (1)...(105); OTHER INFORMATION: CTB variant from NCBI gene bank GI: 2781121 (Ogawa; OTHER INFORMATION: 41).
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 7; Conserv
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APPLICANT: Handley, Harold H.
                                                                                            Query Match
Best Local S
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                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(103)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 494265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 103
TYPE: PRT
                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Vibrio cholera
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                LENGTH:
52 EVPGSQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 EVPGSQH
                                      1 EVPGSQH 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVPGSQH 7
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                                                                          l Similarity
7; Conserv
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                                                                          100.0%; llarity 100.0%; Conservative 0
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  58
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                                                                        Score 39; DB 6
Pred. No. 0.81;
Mismatches
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Pred. No. 0.79;
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                                                                                                                Length 105;
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RESULT 6 US-10-110-364-17 ; Sequence 17, Application US/10110364

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APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: DCT/US00/27607
PRIOR APPLICATION NUMBER: DCT/US00/27607
PRIOR FILING DATE: 1909-10-08
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEO ID NOS: 31
PRIOR FILING DATE: 1999-10-08
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; NAME/KEY: VARIANT;
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1395122
US-10-110-364-17
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                                                                                                                                                                    ; FEATURE:
, NAME/KEY: VARIANT
; LOCATION: (1)...(123)
; OTHER INFORMATION: LTB variant from NCBI gene bank GI: 223254.
US-10-110-364-20
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; Sequence 20, Application US/10110364
; GENERAL INFORMATION:
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Best Local Similarity
Thes 7; Conserv
                                                                     Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
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APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
EILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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PRIOR FILING DATE: 2000-10-05
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TYPE: PRT
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                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                   ORGANISM: Escherichia coli
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71 EVPGSQH 77
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                                    1 EVPGSQH 7
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                                                                             Conservative
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Pred. No.
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Pred. No. 0.
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                                                                                           DB 6; Length 123;
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                        ; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(124)
; OTHER INFORMATION: CTB variant from NCBI
US-10-110-364-6
                                QY
                                                      Query Match
Best Local Similarity
Thes 7; Conserve
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Best Local Similarity
Thehes 7; Conserve
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE DEPERENCE: ACCUSTO
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SEQ ID NO 2
LENGTH: 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haaparanta, Taplo
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED.
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILLING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08
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                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Vibrio cholera
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                                                                                                                                                                                                                                                                                                             LENGTH: 124
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72 EVPGSQH 78
                                    1 EVPGSQH 7
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                                                                          Conservative
                                                                                             100.0%;
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                                                                                             Score 39;
Pred. No.
                                                                                               0.96;
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PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 11
LENGTH: 124
TYPE: PRT
ORGANISM: Vibrio cholera
                                                          Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 7; Conservative 0
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Best Local Similarity
Matches 7; Conserv
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CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karia L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION UNMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
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APPLICANT: Haaparanta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/27607 PRIOR FILING DATE: 2000-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Handley, Harold H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/158,561 PRIOR FILING DATE: 1999-10-08
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                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1169505.
                                                                                                                                                                                                                                                       LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: CTB val
OTHER INFORMATION: 569B).
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1 EVPGSQH 7
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Pred. No. 0
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0.96;
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Best Local S
Matches 7
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
APPLICANT: Happaranta, Tapio
APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
BOATOR AND TOWNSTON NUMBER: US/10/110,364
                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/10110364 GENERAL INFORMATION:
Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/110,364

CURRENT FILING DATE: 2002-04-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: 60/158,561
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                                                                                                   FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(124)
OTHER INFORMATION: LTB variant from NCBI gene bank GI: 1648865
OTHER INFORMATION: (LT87).
                                                                                                                                                                                                        LENGTH: 124
TYPE: PRT
ORGANISM: Escherichia
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TYPE: PRT
ORGANISM: Escherichia coli
FEATURE:
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72 EVPGSQH 78
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Ewalt, Karla L.
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100.0%;
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Pred.
39;
No.
DB 6;
0.96;
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APPLICANT: HABDATANTA, TAPIO
APPLICANT: EWALT, KATIA L.
TITLE OF INVENTION: AB5 TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCT/US00/27607
PRIOR FILING DATE: 2000-10-05
PRIOR FILING DATE: 1999-10-08
NUMBER OF SED ID NOS: 31
SOFTWARE: FastSED for Windows Version 4.0
TYPE: PRT
TYPE: PRT
; NAME/KEY: VARIANT

: LOCATION: (1)...(124)

: OTHER INFORMATION: LTB variant from NCBI gene bank GI: 69630.

US-10-110-364-23
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SOFTWARE: FRASTSEQ for Windows Version 4.0
SEQ ID NO 21

LENGTH: 124
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GENERAL INFORMATION:
APPLICANT: Handley, Harold H.
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APPLICANT: Ewalt, Karla L.
TITLE OF INVENTION: ABS TOXIN B SUBUNIT MUTANTS WITH ALTERED
TITLE OF INVENTION: CHEMICAL CONJUGATION CHARACTERISTICS
FILE REFERENCE: ACTBIO.004A
CURRENT APPLICATION NUMBER: US/10/110,364
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION UMBER: PCT/US00/27607
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR APPLICATION NUMBER: 60/158,561
PRIOR FILING DATE: 1999-10-08
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Query Match
Best Local Similarity 100.0%; Score 39; DB 6; Length 124;
Best Local Similarity 100.0%; Pred. No. 0.96;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 EVPGSQH 7
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Db 72 EVPGSQH 78
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Search completed: July Job time: 652 sec

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
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Perfect score:
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3: pir3:*
4: pir4:*
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Gapop 10.0 ,
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39
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A37133
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T29041
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S44886
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A; Reference number: S17665; MUID: 91355224
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Result No.

Minimum DB Maximum DB

Database

Searched:

Sequence:

Run on:

hypothetical prote	T44138	N	440	76.9	30	5
flavocytochrome C	В70321	N	436	76.9	30	4
hypothetical prote	A89761	N	431	76.9	30	w
hypothetical prote	T47142	2	412	76.9	30	2
chorismate synthas	S17246	Н	376	76.9	30	_
probable 3-oxoadip	T35015	N	375	76.9	30	0
probable 4-carboxy	T47115	N	373	76.9	30	ف
DNA-directed RNA p	A72247	2	336	76.9	30	8
hypothetical prote	F84169	N	304	76.9	30	7
interleukin-7 rece	B34791	2	298	76.9	30	ō
hypothetical prote	AI2241	2	291	76.9	30	G
conserved hypothet	D83072	2	270	76.9	30	4
interleukin-7 rece	C34791	N	262	76.9	30	ũ
conserved hypothet	D83638	Ν	182	76.9	30	2
hypothetical prote	T31701	N	153	76.9	30	ü
hypothetical prote	B72782	2	148	76.9	30	ö

A;CrossTelerences: EMBL:X/6390; NID:g433856; PIDN:CAA539/3.1; PID:g43385/ A;Accession: S39241 A;Molecule type: DNA A;Residues: 1-124 <lew> A;Residues: 1-124 <lew> A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; PID:g433861 A;Cross-references: EMBL:X76391; NID:g433859; PIDN:CAA53976.1; Dodson, Chardson, D.; Ermolaeva, M.D.; Venter, J.C.; Fraser, C.M. R;Reidence of L.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae A;Reference number: A82035; MUID:20406833 A;Accession: H82196 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-124 <heid (59)-1)))="" (7,="" (9,="" 01;="" 1-20="" 1993="" 23-31="" 23-38="" 395-399,="" 40-40="" 51-67="" 60-124="" 9,="" a;crussion:="" a;experimental="" a;molecule="" a;reference="" a;residues:="" a;rolecule="" a;sthi,="" a;title:="" analysis="" biochem.="" biotype="" c.;="" c.h.;="" cao,="" chinese="" classical="" dna="" dna<="" el="" encoding="" gene="" j.s.;="" j:="" jc1078="" ma,="" n16961;="" nucleotide="" number:="" of="" q.j.="" sequence="" serogroup="" source:="" strain="" th="" the="" tor="" type:="" zhang,=""><th>cursor VC1456 [validated] - Vileta chain vision 01-Sep-2000 #text_change 241; H82196; JC1078; S17666; PC 7, March 1991 cholera toxin nucleotide seque cholera toxin nucleotide seque 25 NID:g48420; PIDN:CAA41593.1; i 25 27, November 1993 angement of the Cholera toxin cangement of the Cholera toxin companies.</th><th>35 30 76.9 291 2 AI2241 hypothetical prote 36 30 76.9 298 2 B34791 interleukin-7 rece 37 30 76.9 304 2 F84169 hypothetical prote 38 30 76.9 336 2 A72247 by probable 4-carboxy 40 30 76.9 375 2 T35015 probable 4-carboxy 41 30 76.9 376 1 S17246 chorismate synthas 42 30 76.9 412 2 T47142 hypothetical prote 43 30 76.9 436 2 B70321 flavocytochrome C 440 30 76.9 440 2 T44138 hypothetical prote 6 hypothetical prote 6 ALIGNMENTS</th></heid></lew></lew>	cursor VC1456 [validated] - Vileta chain vision 01-Sep-2000 #text_change 241; H82196; JC1078; S17666; PC 7, March 1991 cholera toxin nucleotide seque cholera toxin nucleotide seque 25 NID:g48420; PIDN:CAA41593.1; i 25 27, November 1993 angement of the Cholera toxin cangement of the Cholera toxin companies.	35 30 76.9 291 2 AI2241 hypothetical prote 36 30 76.9 298 2 B34791 interleukin-7 rece 37 30 76.9 304 2 F84169 hypothetical prote 38 30 76.9 336 2 A72247 by probable 4-carboxy 40 30 76.9 375 2 T35015 probable 4-carboxy 41 30 76.9 376 1 S17246 chorismate synthas 42 30 76.9 412 2 T47142 hypothetical prote 43 30 76.9 436 2 B70321 flavocytochrome C 440 30 76.9 440 2 T44138 hypothetical prote 6 hypothetical prote 6 ALIGNMENTS
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 22-38,'H',40-42,'N',44-67,'T',69,'E',71-90,'N',92-124 <LAI>A;Rote: the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and the difference at residue 70 may be due to deamidation during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during particles and during part
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J. Biol. Chem. 252, 7257-7264, 1977
A:Title: Covalent structure of the beta chain
A:Reference number: A01819; MUID:78005537
A:Accession: A01819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: S17666
A;Molecule type: DNA
A;Residues: 1-38,'H',40-67,'T',69-124 <DA2>
A;Cross-references: EMBL:X58785; NID:g48888; PIDN:CAA41591.1; PID:g48890
R;Ma, Q.J.; Liu, C.X.; Xiong, L.S.; Yu, X.Q.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 34, 274-280, 1991
A;Title: B subunit of cholera toxin produced in Escherichia coli.
A;Reference number: PC1010
A;Accession: PC1010
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A:Title: Determination of the primary structure
A;Reference number: A38033; MUID:78005536
A;Accession: A38033
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A; Residues: 1-32,'S',34-74,'S',76-124 <MEK>
A; Cross-reference: GB:X00171; NID:g48347; PIDN:CAA24996.1; PID:g758351
Вb
                                                                                                                                                                                                                                                                                                                                      F;1-21/Domain: signal sequence *status predicted <SIG>F;22-124/Product: cholera enterotoxin chain B \#status F;30-107/Disulfide bonds: \#status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: involved in binding C; Superfamily: cholera enterotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ciate noncovalently
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Complex: the cholera enterotoxin molecule contains ciate noncovalently with the subunit B, an aggregate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Mesidues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103,
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103,
A;Residues: 22-38,'H',40-67,'T',69,'E',71,'QS',74-75,'VE',78-86,'Q',88-99,'Q',101-103,
A;Reference number: A1930; MUID:85126976
A;Reference number: A21910; MUID:85126976
A;Recession: A21910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Primary structure of the B subunit of cholera enterotoxin. A;Reference number: A38034; MUID:77026365
A;Accession: A38034
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A; Residues: 22-38, 'H', 40-42, 'N', 44-67, 'T', 69-90, 'N', 92-124
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A;Reference number: A93320; MUID:84068199
                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: enterotoxin; toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: VC1456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Comment: The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein
A; Residues: 22-38,'H', 40-42,'N', 44-67,'T', 69-90,'N', 92-124
A; Experimental source: biotype Inaba 569B
A; Note: Asn-65 was partially deaminated to Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R; Lai, C.Y.
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                                                                                                                                                                               Query Match
Best Local
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72
                                                                           \vdash
                                                                           EVPGSQH 7
EVPGSQH 78
                                                                                                                                                   Similarity 7; Conser
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Pred. No. 0.5
0; Mismatches
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beta chain
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Qy

EVPGSQH

Query Match Best Local S Matches 7

Similarity

100 .08; 0,

Score 39; Pred. No. Mismatches

0

0,

Indels

0;

Gaps

0

), 5; Bg (5),

Length 124;

Conservative

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R;Inoue, T.; Tsuji, T., Koto, M.; Imamura, S.; Miyama, A. FEMS Microbiol. Lett. 108, 157-161, 1993
A;Title: Amino acid sequence of heat-labile enterotoxin from A;Reference number: 153542; MUID:93252225
A;Accession: I67644
A;Status.
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A;Residues: 1-5,'F',7-17,'C',19-24,'S',26-27,'E',29-33,'H',35-63,'K',65-66,'A',68-122
A;Cross references: GB.M17874; NID:g145830; PIDN:AAA98064.1; PID:g145831
A;Experimental source: plasmid ENT-R PCG86
R;Ibrahimi, I.; Gentz, R.
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-17, (C',19,'Y',21-24,'S',26-27,'E',29-63,'K',65-66,'A',68-122,'E',124
A; Cross-references: GB: $60731; NID: 9408994; PIDN: AAC60441.1; PID: 9408996
R; Tsuji, T.; Lida, T.; Honda, T.; Miwatani, T.; Nagahama, M.; Sakurai, J.; Wada, K
Microb. Pathog. 2, 381-390, 1987
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                                                                                                                                                                                                    A; Molecule type: protein A; Molecule type: protein A; Experimental source: strain 240-3 C; Complex: the heat-labile enterotoxin molecule contains one A chain and five
                                                                                                                                                                                                                                                                                                                     A;Title: A unique amino acid sequence of the B subunit of a heat-labile enterotoxin A;Reference number: A61475; MUID:89180953 A;Accession: A61475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-27, 'E', 29-63, 'K', 65-124 <YAM>
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Nature 288, 499-501, 1980
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F;1-21/Domain: signal sequence *status predicted <SIG>F;22-124/Product: heat-labile enterotoxin chain B *staF;30-107/Disulfide bonds: *status predicted
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A;Accession: I41287
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                                                                                         C; Keywords: enterotoxin
                                                                                                                    A;Description: the biological activity of the toxin C;Superfamily: cholera enterotoxin beta chain
                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
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Chem. 262, 10
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conserved hypothetical exported protein SMb20700 [imported] - Sinorhizobium meliloti
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30'Sep-2001
C;Accession: G96017
               R; Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A; Title: The complete sequence of the 1,683-kb psymB megaplasmid from the N2-fixing ender, Reference number: A95842; MUID:21396508; PMID:11481431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: Over-expression A; Reference number: Z14418 A; Accession: T01751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N;Alternate names: Ntc16 protein
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 20-Jun-2000
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C; Superfamily:
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C;Accession: T14755
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A; Residues: 1-272 <WAM>
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5; Conserv
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85.7%;
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71.48;
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Pred. No. 22;
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EVPGGEH

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Nature 390, 249-256, 1997

A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Galizzi, A; Gal A; Authors: Foulger, D; Fritz, C; Fujita, M; Fujita, Y; Fuma, S; Hosono, S; Hullo, M Koetter, P; Koningstein, G; Krogh, S; Kumano, M; Kurita, K; Lapidus, A; Lardino A; Authors: Lauber, J; Lazarevic, V; Lee, S, M; Levine, A; Liu, H; Masuda, S; Mau Y, M; Ogawa, K; Ogiwara, A; Oudega, B; Park, S.H; Parro, V; Pohl, T.M; Portete Rleger, M; Rivolta, C; Rocha, E; Roche, B; Rose, M; Sadaie, Y; Sato, T; Scanl A; Authors: Schleich, S; Schroeter, R; Scoffone, F; Sekiquchi, J; Sekowska, A; Se akeuchi, M; Tamakoshi, A; Tanaka, T; Terpstra, P; Tognoni, A; Tosato, V; Uchiya T; Winters, P; Wipat, A; Yamamoto, H; Yamane, K; Yasumoto, K; Yata, K; Yoshida A; Atthors: Yoshikawa, H.F; Zumstein, E; Yoshikawa, H; Danchin, A. A; Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili A; Reference number: A69580; MUID:98044033
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R.Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glucarate dehydratase (EC 4.2.1.40) - Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:Z99105; GB:AL009126; NID:g2632457; PIDN:CAB12043.1; PID:g26325
A;Experimental source: strain 168
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A; Residues: 1-137 < KUR>
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A;Residues: 1-455 <KUN>
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Best Local S
Matches 6
                                                                                                                                                                                                           Superfamily: glucarate dehydratase; Superfamily: glucarate dehydratase; hydro-lyase
                                                                                          Query Match
Best Local
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5; Conser
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71.48;
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Pred. No.
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Pred. No.
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glutamate synthase (NADPH) (EC 1.4.1.13) small chain [imported] - Yersinia pestis (sc;Species: Yersinia pestis
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG0432
R;Parkhill, J: Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre, Nature 413, 523-527, 2001
                                                                                                                                                                    C;Species: Mycobacterium leprae
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change
C;Accession: B27586
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                   A; Molecule type: DNA
A; Residues: 1-137 < BOO>
                                                               A; Reference number: A; Accession: B27586
                                                                                   A; Title: Antigenic proteins A; Reference number: A92821;
                                                                                                                           R;Booth, R.J.; Harris, D.P.; Love, J.M.; Watson, J.D. J. Immunol. 140, 597-601, 1988
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A;Molecule type: DNA
A;Residues: 1-534 <DUZ>
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A;Description: Sequence of the C. elegans cosmid ZK112.
A;Reference number: S44616
A;Accession: S44886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZK112.1 protein - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
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C;Keywords: oxidoreductase
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A;Molecule type: DNA
A;Residues: 1-472 <KUR>
A; Cross-references:
                                                                                                                                                                                                                                    hypothetical protein - Mycobacterium leprae
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lly: Caenorhabditis elegans ZK688.6 protein
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GB:M19058; NID:g149919;
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ns of Mycobacterium leprae. Complete
1; MUID:88088878
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71.48;
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57.1%;
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  PIDN: AAA88230.1;
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A; Authors: Hunter, J.L.; Jenkins, J.J.; Johnson-Hopson, C.; Khan, S.; Khay C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Mait Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wonder, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein F20B17.2 (imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B. submitted to the EMBL Data Library, August 1998 A;Reference number: 221556
A;Accession: T34'67
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Query Match
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A;Gene: SCOEDB:SC2All.21c
                                                                                                              A; Gene: F20B17.2
A; Map position:
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                                                                                                                                                        C; Genetics
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                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-260 <STO>
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A; Residues: 1-242 <MUR>
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ce: strain A3(2)
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                                     31;
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Maiti, R.
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RESULT 14
H75446
(S)-2-hydroxy-acid oxidase - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-JI
C;Accession: H75446
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson,
N.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback,
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A;Molecule type: nucleic acid
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Dev. Biol. 154, 55-65, 1992
A;Title: Two distal-less re
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C:Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C:Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 24-Sep-1999
C:Accession: B48820
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A;Molecule type: DNA
A;Residues: 1-274 <STO>
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A48820; MUID:93050784
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71.4%;
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                                                                               J.D.; Dodson,
T.; Zalewski,
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Search completed: Job time: 232 sec

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R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.;
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.;
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                            conserved hypothetical protein TC0328 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 1
C;Superfamily: (S)-2-hydroxy-acid c
F;3-297/Domain: (S)-2-hydroxy-acid
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A; Residues: 1-353 <WHI>
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                                                                                                                                                                              A;Cross-references: GB:AE002300; GB:AE002160; NID:g7190365; PIDN:AAF39192.1; PID:g719
A;Experimental source: strain Nigg (MoPn)
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A; Residues: 1-374 <TET>
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A;Experimental source: strain R1
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A;Accession: D81715
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homology <2HY>
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          protein search, using
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12.601 Million cell updates/sec
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P34610 caenorhabdi
P34610 saenorhabdi
Q9z183 mus musculu
Q61045 mus musculu
P13733 mycobacteri
Q60543 homo sapien
P58009 thermotoga
P53770 notophthalm
Q91284 pleurodeles
Q90229 ambystoma m
Q9ttr7 bos taurus
P24468 homo sapien
P43135 mus musculu
Q12640 neurospora
P16872 mus musculu
Q62406 mus musculu
Q62406 mus musculu
Q77989 thermotoga
P16871 thermotoga
P28777 saccharomyc
P16871 homo sapien
P80404 homo sapien
P18487 drosophila
Q16671 homo sapien
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ALIGNMENTS

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Fraser C.
                                                                                                                                                                                                                                                                    entities requires a license agreement (S or send an email to license@isb-sib.ch).
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"Structural studies of receptor binding by Protein Sci. 6:1516-1528(1997).
-i- FUNCTION: THE BETA CHAIN AGGREGATE (B
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STRAIN-OGAWA 41 / CLASSICAL BIOTYPE;
MEDLINE-97376625; PubMed-9232653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang R.G., Westbrook M.L., Westbrook E Maulik P.R., Reed R.A., Shipley G.G.;
"The 2.4 A crystal structure of cholera
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MEDLINE=78005537; F
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SUBUNIT: CONTAINS 3 KINDS OF CHAINS. AN ALPHA AND A GAMMA CHAIN (FROM THE SAME PRECURSOR MOLECULE), LINKED BY AN INTERCHAIN DISULFILE BOND, ASSOCIATE NONCOVALENTLY WITH AN AGGREGATE OF 4 T6 BETA CHAINS.
                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Encuropean Bioinformatics Institute. There are no restroy by non-profit institutions as long as its content
                                                                                                                                               X00171; CAA2496.1; -.

K01170; AAA27573.1; -.

J030053; BAA06291.1; -.

X58786; CAA41593.1; -.

X76391; CAA53973.1; -.

X76391; CAA53973.1; -.

X76391; CAA53976.1; -.
                             1CHQ;
1FGB;
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3СНВ;
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08-MAR-96.
08-MAR-96.
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MEDLINE=85156481; PubMed=3884513;
Leong J., Vinal A.C., Dallas W.S.;
                     Yamamoto T., Tamura T.A., Yokota T., T
"Overlapping genes in the heat-labile
from Escherichia coli human strain.";
                                                           STRAIN=ISOLATE H10407;
MEDLINE=83114628; PubMed=6759877;
                                                                                                                                 "Nucleotide sequence comparison between cistrons from Escherichia coli of human
                                                                                                                                                                                                                                                          Escherichia coli.
Bacteria; Proteobacteria;
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Pfam; PF01376; Enterotoxin_B; 1.
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72 EVPGSQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93252225; PubMed-8486242; Inoue T., Tsuji T., Koto M., Imamura S., Miyama A.; "Amino acid sequence of heat-labile enterotoxin from chicken enterotoxigenic Escherichia coli is identical to that of human strain H 10407.";
                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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1- FUNCTION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL
-1- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE
                                                                                                                                                                                                                                                                                                                                           EMBL; M17874; AAA98064.1; -.
EMBL; J01646; AAB02982.1; -.
EMBL; S60731; AAC60441.1; -.
EMBL; X83966; CAA58800.1; -.
EMBL; X83966; CAA58800.1; -.
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MEDLINE=99185101; PubMed=10085117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISCUSSION OF SEQUENCE MEDLINE-95349400; PubMe
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STRAIN-ISOLATE H10407;
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Enterotoxin; Signal; 3D-structure
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MEDLINE-85156481; PubMed-3884513;
Leong J., Vinal A.C., Dallas W.S.;
"Nucleotide sequence comparison be
cistrons from Escherichia coli of
Infect. Immun. 48:73-77(1985).
                                                                                       Domenighini M., Pizza M., Jobling M.G., Holmes R.K., Rappuoli R "Identification of errors among database sequence entries and comparison of correct amino acid sequences for the heat-labile enterotoxins of Escherichia coli and Vibrio cholerae.";
will Microbiol. 15:1165-1167(1995).

MICROBION: THE BIOLOGICAL ACTIVITY OF THE TOXIN IS PRODUCED THE A CHAIN, WHICH ACTIVATES INTRACELLULAR ADENYL CYCLASE.

-!- SUBUNIT: HETEROHEXAMER OF ONE A CHAIN AND OF FIVE B CHAINS.
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Yamamoto T., Gojobori T., Yokota T.;
Yamamoto T., Gojobori T., Sokota T.;
"Evolutionary origin of pathogenic de
Escherichia coli and Vibrio cholerae
J. Bacteriol. 169:1352-1357(1987).
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21-JUL-1986 (Rel. 01, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Heat-labile_enterotoxin B chain precursor (LT-B,
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                             Nature [7]
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MEDLINE=91238966; PubMed=2034287;
Sixma T.K. Pronk S.E. Kalk K.H., War
Witholt B., Hol W.G.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A functional interaction between the signal peptide and the translation apparatus is detected by the use of a single point mutation which blocks translocation across mammalian endoplasmic
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"Amino acid sequence homology between coli heat-labile toxin.";
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STRAIN=ISOLATE P307;
MEDLINE=81074965; Pu
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J. Mol. Biol 230.800.777.
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reticulum.";
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Subtlist; BG11161; gudb.
InterPro; IPR001354; MR_MLE; 1.
Pfam; PF01188; MR_MLE; 1.
Pfam; PF02746; MR_MLE_N; 1.
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microbiology 141:269-275(1995).
-i- FUNCTION: CATALYZES THE DEHYDRATION OF GLUCARATE TO 5-KETO-4-
DEOXY-D-GLUCARATE (5-KDGLUC) (BY SIMILARITY).
-i- CATALYTIC ACTIVITY: D-glucarate = 5-dehydro-4-deoxy-D-glucara
                         This
                                                                            elegans.";
Nature 368:32-38(1994)
-!- SIMILARITY: BELONG
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BRISTOL N2;
MEDLINE-94150718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Putative serine protease
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                                                                       SIMILARITY: BELONGS TO PEPTIDASE FAMILY S28 (SERINE PROTEASE).
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European Bioinformatics Institute
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SIMILARITY: BELOWGS TO THE MANDELATE RACEMASE
LACTONIZING ENZYME FAMILY. GLUCD SUBFAMILY.
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SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
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Mus musculus (Mouse).
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                                                                                              -!- CATALYTIC ACTIVITY: Protein L-arginine
citrulline + NH(3).
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                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; NCBI_TaxID=10090;
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m I}, type III and type IV, and the expression pattern of type I in
                                                                                                                                                                                                                           Takahara H.
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                                                                                                                                           J. Biochem. 259:660-669(1999).
FUNCTION: CATALYZES THE DEIMINATION
                                                 DEIMINASE.
                                                                SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                        Vertebrata; Euteleostomi;
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Best Local :
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                                                                                                   Genome
                                                                                                                                                                                                                                                                                             "Expression patterns of two murine homologs of Drosophila single-minded suggest possible roles in embryonic patterning the pathogenesis of Down syndrome.";
                                                                                                                                                                                                                                                                                                                                 STRAIN-SWISS WEBSTER;
MEDLING-97020303; PubMed-8812055;
Fan C.-M., Kuwana E., Bulfone A.,
Jenkins N.A., Crews S., Martinez
Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
15-JUL-1999 (Rel. 38, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
single-minded homolog 1 (mSIM1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                    Unpublished results, Chrast R., Scott H.S
                                                                                                                                                                                                                            MEDLINE=97029422; PubMed=8875433; Fan C.-M., Kuwana E., Bulfone A., Jenkins N.A., Crews S., Martinez
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                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                          Fan C.-M.;
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Mammalia; Eutheria;
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                                                                MEDLINE=96413339; PubMed=8927054;
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239 ELPGGQH 245
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                                                                                                            R., Scott H.S., Chen H., F., Shimizu N., Antonarakis Res. 7:615-624(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
5; Conserv
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                                                                                                                                                                                                         Neurosci.
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16:5865-5875(1996)
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74476 MW;
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Rodentia;
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Pred. No.
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Sciurognathi; Muridae;
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Ls S.E.;
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S., Puelles L.,
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Puelles
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InterPro; IPR003015; HLH_Myc.
InterPro; IPR001992; HLH_dim.
InterPro; IPR001067; Nuctrnslocator.
InterPro; IPR0010610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS.
Pfam; PF00785; PAC; 1.
Pfam; PF00785; PAS; 2.
Pfam; PF00785; PAS; 2.
SMART; SM00081; PAS; 2.
SMART; SM00091; PAS; 2.
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CONFLICT
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SEQUENCE FROM N
STRAIN=129/SV;
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                                                                                                                                       PROSITE; PS00038; HELI)
PROSITE; PS50112; PAS;
Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Probst M.R., Fan C.M., Tessier-Lavigne M., Hankinson O.; "Two murine homologs of the Drosophila single-minded protein interact with the mouse aryl hydrocarbon receptor nuclear
                                                                                                                            Transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
 SEQUENCE
                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translocator protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOL Chem. 272:4451-4457(1997).
FUNCTION: TRANSCRIPTIONAL FACTOR THAT MAY HAVE PLEIOTROPIC EFFECT:
DURING EMBRYOGENESIS AND IN THE ADULT.
SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
BHLH PROTEIN. HETERODIMER OF SIMI AND ARNT.
TISSUE SPECIFICITY: DETECTED IN LUNG, SKELETAL MUSCLE AND KIDNEY.
DURING FETAL DEVELOPMENT IT IS FOUND IN THE CNS, DEVELOPING
KIDNEY, MESODERMAL AND ENDODERMAL TISSUES, INCLUDING DEVELOPING
KIDNEY, MESODERMAL AND ENDODERMAL TISSUES, INCLUDING DEVELOPING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSCRIPTION FACTORS.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
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SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
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133
176
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 AA;
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B1A7F7DA8578CD17
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 CRC64;
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Query

Match

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Length 765;

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Best Local S
Matches 5
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Matches 6; Conserv
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Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
Barrell B.G.;
 CIDA_HUMAN 060543;
                                                                                                                                                                                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                 Hypothetical protein; Complete proteome. SEQUENCE 137 AA; 15195 MW; 633E68BF3FDAD0BB CRC64;
                                                                                                                                                                                                                                         EMBL; M19058; AAA88230.1; -. EMBL; AL583923; CAC30749.1; PIR; B27586; B27586.
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MEDLINE=88088878; PubMed=2447183;

MEDLINE=88088878; PubMed=2447183;

Booth R.J., Harris D.P., Love J.M., W

Booth R.J., Harris D.P., Love J.M., W

"Antigenic proteins of Mycobacterium

gene for the 18-kDa protein.";

J. Immunol. 140:597-601(1988).
                                                                                                                                                                                                                          Leproma; ML1796; -
                                                                                                                                                                                                                                                                                                                                                                                                   "Massive gene decay in the leprosy bacillus."; Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-TN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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NCBI_TaxID=1769;
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Hypothetical
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01-JAN-1990
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SEQUENCE FACE.

STRAIN-MSIB / DSM 3109;

STRAIN-MSIB / DSM 3109;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.C., Ketchum K.A.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heldelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria fro
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YB5A_THEMA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; l
                                                                                                                                                                                                                                                                                         Thermotoga maritima.
Bacteria; Thermotogales;
COLTAXID=2336;
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16-OCT-2001
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Pfam; PF02017; CIDE-N; 1.
SMART; SM00266; CAD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inohara N., Koseki T., Chen S., Wu X., Nunez G. "CIDE, a novel family of cell death activators kDa subunit of the DNA fragmentation factor."; EMBO J. 17:2526-2533(1998).
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SUBUNIT: INHIBITED BY DFFB.
SIMILARITY: CONTAINS 1 CIDE-N DOMAIN.
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activator CIDE-A (Cell death-inducing DFFA-like effector
                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40,
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Pred. No.
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; 05F704823CE71C0E CRC64;
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P53770;
01-OCT-1996
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                                                                                                           use by non-profit institu modified and this statement entities requires a license
                                                                                                                                                                                                                                                                     Beauchemin M., Savard P.;
"Two distal-less related homeobox-containing regeneration blastemas of the newt.";
Dev. Biol. 154:55-65(1992).
-!- SUBCELLULAR LOCATION: Nuclear (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
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Unpublished observations (APR-2001).
                    InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
Pfam; PF00046; homeobox; 1.
                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                   Notophthalmus viridescens (Eastern newt) (Triturus viridescens)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom
Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last anotation update)
101-NOV-1997 (Rel. 35, Last anotation update)
101-NOV-1997 (Rel. 36, Last anotation update)
                                                             EMBL; X63531; CAA45094.1; -. HSSP; P22808; 1NK3.
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                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skin
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00024; HOMEOBÓX.
PRINTS; PR00031; HTHREPRESSR.
SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicolas S., Massacrier A., Caubit X., Cau P., le Parco Na Distal-less-like gene is induced in the regenerating nervous system of the urodele Pleurodeles waltl."; Mech. Dev. 56:209-220(1996).
                                                                                                                                                                                                                                                                                                    Homeobox; DNA-binding; Developmental protein; Nuclear DNA_BIND 126 185 HOMEOBOX.
                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00027; HOMEOBOX_1; 1. PROSITE; PS50071; HOMEOBOX_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000047; HTH_repressr.
InterPro; IPR001356; Homeobox.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Swiss Institute of Bioinformatics and the Entry between the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics and the Bioinformatics a
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Amphibia; Batrachia;
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Salamandroidea; Salamandridae;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
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01-NOV-1997
30-MAY-2000
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MEDILINE-97108743; PubMed-8951064;

Mullen L.M., Bryant S.V., Torok M.A., Blumberg

"Nerve dependency of regeneration: the role of
signaling in amphibian limb regeneration.";

Development 122:3487-3497(1996).

-!- SUBCELLULAR LOCATION: Nuclear (Potential).

-!- SUBCELLULAR EDCATION: THE DISTAL-LESS FAMI
                Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
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PRINTS; PR00031; HTHREPRESSR
SMART; SM00389; HOX; 1.
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                                                                                                                                                                                                                                                                                                                                                  189
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InterPro; IPR001356; Homeobox.
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                     Pecora; Bovoidea;
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Matches 6
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COT2_HUMAN STANDARD; PRT; 414 AA.

P24468; Q03754;

01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
COUP transcription factor 2 (COUP-TF2) (COUP-TF II) (Apolipoprotein regulatory protein-1) (ARP-1).

NR2F2 OR TFCOUP2 OR ARP1.
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InterPro; IPR001723; Strdhormone_receptor.
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
PRINTS; PR00398; STRDHORMONER.
PRINTS; PR00398; STRDHORMONER.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; E
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Ladias J.A.A., Karathanasis S.K.; "Regulation of the apolipoprotein AI gene the steroid receptor superfamily.";
                                                                                                   SEQUENCE FROM N.A. MEDLINE=91118002; PubMed=1899293;
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Transcription regulation; DNA-binding; Nuclear protein;
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SM00399; ZnF_C4; 1.
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EMBL; U60477; AAB09475.1; -.
EMBL; M62760; AAA21479.1; -.
PIR; A37133; A37133.
HSSP; P19793; 2NLL.
TRANSPAC; T00045; -.
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ZN_FING
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DOMAIN
SEQUENCE
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PRINTS; PR00047; STROIDFINGER.
SMART; SM00430; HOLI; 1.
SMART; SM00399; ZnF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000536; Hormone_r
InterPro; IPR001723; Strdhormo
InterPro; IPR001628; zf-C4.
Pfam; PF00104; hormone_rec; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Expr. 1:207-216(1991).

- IF FUNCTION: REGULATION OF THE APOLIPOPROTEIN

- BINDS TO DAN SITE A.

- I- SUBUNIT: BINDS DNA AS AN HOMODIMER.

- I- SUBCELLULAR LOCATION: Nuclear.

- I- TISSUE SPECIFICITY: FOUND IN ALL TISSUES.

- I- TISSUE SPECIFICITY: FOUND IN ALL TISSUES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Speckmayer R.W.M., Possibmitted (OCT-1996)
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EVPGSQ
                                                                                          Similarity 6; Conserv
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PS00031; NUCLEAR_RECEPTOR;
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DNA-binding;
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EMBL/GenBank/DDBJ
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NUCLEAR R
C4-TYPE.
C4-TYPE.
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Pred. No.
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related transcription
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                         Q9r646 vibrio chol
Q57193 vibrio chol
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Q57215 vibrio chol
Q56635 vibrio chol
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Q93v32 escherichia
Q94m01 vibrio phag
Q22511 vitis vinif
Q9w7d3 oryzias lat
Q9w7d4 oryzias lat
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Q9r728 streptomyce
Q9npq6 homo sapien
Q9ug04 homo sapien
Q9ug04 nicotiana t
          Q9y2b3 homo sapien
Q9vfe2 drosophila
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 Q9fqi8 amaranthus
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Q9R646

Q9R646; Q9R646

PRELIMINARY;

103

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHOLERA-LIKE ENTEROTOXIN B SUBUNIT.
Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

Microbiol. Immunol. 39:87-94(1995). HSSP; P01556; 1XTC.

SEQUENCE.
MEDLINE=95303036; PubMed=7783690;
Nakashima K., Eguchi Y., Nakasone N.;
"Characterization of an enterotoxin p

produced by Vibrio cholerae

NCBI_TaxID=666;

0139."

ALIGNMENTS

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RESULT
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Q57193
Q57193;
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Pfam; PF01376; Enterotoxin_B; 1.

PRINTS; PR00772; ENTEROTOXINB.

ProDom; PD012805; Enterotoxin_B; 1.

SEQUENCE 103 AA; 11645 MW; 992A05C077F2F70E CRC64;
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51 EVPGSQH 57
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      PRELIMINARY;
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                                                                             Score 39; DB 2; Length 103; Pred. No. 0.53;
      PRT;
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RESULT

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Best Local :
EMBL; AF1/5/00, HSSP; P01556; 2CHB.
HSSP; P01556; 2CHB.
InterPro; IPR001835; Enterotoxin_B.
Pfam; PF01376; Enterotoxin_B; 1.
PRINTS; PR00772; ENTEROTOXINB.
                                                                                                                                                                                                                                                                                                                                                                           Q9RP15;
Q9RP15;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                      SEQUENCE FROM N.A.

STRAIN-KNIHOO2;
Shin H.J., Park Y.C., Kim Y.C.;
Shin H.J., Park Y.C., Kim Y.C.;
"Cloning and nucleotide sequence analysis of the cassette from Vibrio cholerae KNIHOO2 isolated in Misainmurhag Hoiji 35:205-210(1999).

EMBL; AF175708; AAD51360.1;
TELECTROPIESE Extractions
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01-NOV-1996
01-JUN-2001
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                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                 Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                        CTXB.
                                                                                                                                                                                                                                                                                                                                                         CHOLERA ENTEROTOXIN
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EMBL; A00931; CAA00098.1; --
HSSP; P01556; 2CHB
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STRAIN-CLASSICAL BIOTYPE 569B;
Shi C., Cao C., Zhang J., Ma Q.;
Chin. Blochem. J. 9:395-399(1993).
                                                                                                                                                                                                                                                                          NCBI_TaxID=666;
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STRAIN=CLASSICAL BIOTYPE
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MEDLINE-91355224; PubMed-1883840;
Dams E., De Wolf M., Dierick W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1090:139-141(1991).
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7; Conservative
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(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
EROTOXIN B-SUBUNIT.
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(CTB) PRECURSOR (CTB).
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Pred. No. 0.6
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Best Local
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                Komase K.,
Submitted
[2]
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SIGNAL
 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                   Q93V32;
01-DEC-2001
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"Comparison of cholera toxin strains 854 (0139-bengal) and Submitted (APR-1994) to the F
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01-NOV-1996 (Tremblrel.
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CHOLERA TOXIN PRECURSOR.
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                                                                                        SEQUENCE FROM N.A.
                                                                                                                       NCBI_TaxID=562;
                                                                                                                                                              Bacteria;
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RESULT
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Best Local S
Matches 7
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Best Local S
Matches 7
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-CV. THOMPSON SEEDLESS (CLONE 2A); .
Cassol T., Adams D.O.;
"Cloning of a grape glutathione reductase
"Cloning of a grape glutathione reductase
                                                                                                                                                      022511
022511;
01-JAN-1998
01-JAN-1998
01-DEC-2001
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01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine 12:1083-1089(1994).
Vaccine 12:1083-1089(1994).
EMBL; AB011677; BAA25726.1; -.
EMBL; AB011677; BAA25726.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q94M01;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

Bhattacharyyaa T., Nandy R.K., Nair G.B.;

"The entire core region of the ctx-phi (ctx-prophage) in environmental strain of V. cholerae.";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF414369; AAL09682.1; -.

SEQUENCE 124 AA; 13884 MW; 8D4C251591B16891 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio phage CTX.
Viruses; ssDNA viruses;
NCBI_TaxID=141904;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTXB.
                                                                                                Vitis vinifera (Grape).
Eukaryota; Viridiplantae; Stro
Spermatophyta; Magnoliophyta;
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                                                                            NCBI_TaxID=29760;
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MEDLINE=95091056; PubMed=7998417;
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trace amount of
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Similarity 100
7; Conservative
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(TrEMBLrel. 19, Last annotation updat
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                                                                                                Streptophyta; Embryophyta; Tracheophyta; /ta; eudicotyledons; core eudicots; Vitaceae;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                  Score 39; DB
Pred. No. 0.6
); Mismatches
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Pred. No. 0.6
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T., Aizawa C.,
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C., Oya A.,
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AC Q9
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Q9W7D3
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Matches 5
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Q9W7D3;
01-NOV-1999 (TrEMBLrel. 1
01-NOV-1999 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
    Q9W7D4 PRELIMINARY; PRT; 199 AA. Q9W7D4; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat HYPOTHETICAL 21.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                Oryzias latipes (Medaka fish).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;

Beloniformes; Adrianichthyldae; Oryzinae; Oryzias.
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Pfam; PF02852; pyr_redox_dim; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
PRINTS; PR00469; PNDRDTASEII.
PROSITE; PS00076; PYRIDINE_REDOx_1;
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ORANGE-RED;
MEDLING-20070874; PubMed-10602271;
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                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                           "Systematic identification of genes in medaka.";
                                                                                                                                                                                                                                                                                    Kanamori A.;
                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8090;
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ilarity 100.0%;
Conservative (
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71
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pyr_redox.
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Pred. No.
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Oryzias latipes

(Medaka fish)

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MEDLINE=97000351; PubMed=8843436;
Redenbach M., Kleser H.M., Denapaite D., Eichner A., Cullum J.,
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                                                                                     the 8 Mb Streptomyces coelicolor A3(2) chromosome.
MO1. Microbiol. 21:77-96(1996).
EMBL; AL133210; CAB61584.1; -.
InterPro; IPR002502; Amidase_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oliver K., Harris D.;
Submitted (NOV-1999)
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n-atamia: Firmicutes; Actinobacteria; Actinobacteridae;
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01-MAY-2000 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
PUTATIVE AMIDASE.
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STRAIN=ORANGE-RED;
MEDLINE=20070874; PubMed=10602271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cerdeno A.M., Parkhi
Submitted (NOV-1999)
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Oliver K., Ha
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Mol. Reprod. Dev. 55:31-36(2000).
EMBL; AF128817; AAD38914.1; -.
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SEQUENCE 199 AA; 21726 MW;
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"Systematic identification of genes
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176
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                                      EVPGSQH
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EVPGSDH
                                                                                                                                                                                                PF01510;
                                                                                   Similarity 6; Conserv
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                                                                                      Conservative
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182
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V-1999) to the
                                                                                                                                                                                              Amidase_2;
AA; 22749
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85.7%;
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9 MW;
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e EMBL/GenBank/DDBJ databases
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Last annotation updat
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Pred. No.
                                                                                                          Score 34; DB Pred. No. 14;
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SEQUENCE 272 AA; 31016 MW;
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Q9UG04;
01-MAY-2000
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Q9NPQ6;
01-OCT-2000
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 31.0 KDA PROTEIN (UNKNOWN) (PROTEIN FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Auffray C., Ansorge W., Ballabio A. Lehrach H., Poustka A., Lundeberg J "The European IMAGE consortium for human gene transcripts.";
Submitted (JUL-2000) to the EMBL/Ge EMBL; AL389957; CAB97531.1; -.
                                                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                                             TISSUE=BRAIN, NEUROBLASTOMA;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                 TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DKFZP564A0122
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Mammalia; Eutheria;
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01-OCT-2000
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r-2000 (TrEMBLrel. 15, Last annotation u
LCAT-LIKE LYSOPHOSPHOLIPASE (FRAGMENT).
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5; Conserv
Similarity
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R., Estivill X., Escarceller M., Sum
(JUL-2000) to the EMBL/GenBank/DDBJ
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(TrEMBLrel. 15, 1)
(TrEMBLrel. 15, 1)
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84.6%;
71.4%;
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Pred.
Score 33; DB Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; I Catarrhini; Hominidae;
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                     Length 272;
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080418;
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EMBL; ABO17494; BAA76877.1; -...
InterPro; IPR003386; LACT.
Pfam: PF02450; LACT; 1...
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Taniyama Y., Shibata S., Kita S., Horikoshi K., Sumino Y., Fujino M.;
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Mammalia; Eutheria;
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"Over-expression of a tobacco homeobox gene, NTH15, dec
expression of a gibberellin biosynthetic gene encoding
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Bottchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Bottchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Codson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., J. Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
RA Dodson K., J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
RA Dodson K., J., Evangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
RA Dodson K., J., Brangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., McIntosh T.C., McLeod M.P., McPherson D.,
RA Kimmel B.E., Siden-Kiamos I., Simpson M., McHerod M.P., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Kelchum K.A., Weinstock G.M., Weissenbach J.,
RA Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Kelchum K.A., Moodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Kanna K.M., Woodage T., Worley K.C., Wu D., Yang S., Zhu X., Smi
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                   Recep_L_domain; AA; 98349 MW;
                               84.6%;
71.4%;
                                                                                                                                                                                                                                                                 CG3837.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13,
13,
17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence up
Last annotation
                               Score 33; DB 5;
Pred. No. 1.1e+02;
                                                                                                                                                                   2.
F6562A64E72E7B21 CRC64;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Champe M., Pfeiffer B.D.,
   0;
                                                           Length 868,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iklos G.L.G.,
Baldwin D.,
0;
Gaps
0
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